CLAIMS

We claim:

1. A biochip comprising a solid substrate comprising an array comprising:

a) at least one capture probe substantially homologous to a portion of the sense strand of a nucleic acid encoding CPY1A1;

b) at least one capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY1A2;

c) at least one capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY1B1;

d) at least one capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY2C19;

e) at least one capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY2D6;

f) at least one capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY2E1; and

g) at least one capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY3A4.

2. A biochip according to claim 1 wherein said first portion of said sense strand of said nucleic acid encoding CPY2D6 is adjacent to a single nucleotide polymorphism (SNP) position of interest.

3. A biochip according to claim 1 wherein said first portion of said sense strand of said nucleic acid encoding CPY2D6 includes at a terminus a single nucleotide polymorphism (SNP) position of interest.

4. A biochip according to claim 1 wherein said array further comprises at least one capture probe substantially homologous to a portion of the antisense strand of a nucleic acid encoding a protein selected from the group consisting of CYP1A1; CYP1A2; CYP1B1; CYP2C19; CYP2D6; CYP2E1 and CYP3A4.

5. A biochip according to claim 1 wherein said array further comprises at least one capture probe substantially homologous to a portion of a CYP pseudogene.

6. A biochip according to claim 1 wherein said solid support is selected from the group consisting of glass, plastic, ceramic, and PC board.

7. A biochip according to claim 1 wherein said array comprises an array of electrodes.

8. A biochip according to claim 1 wherein said array comprises an array of polymer gel pads.

9. A method of determining the identification of a nucleotide at a detection position in at least one target sequence selected from the group consisting of CYP1A1, CYP1A2, CYP1B1, CYP2C19, CYP2D6, CYP2E1 and CYP3A4, said method comprising:

a) providing an array comprising:

i) at least one first capture probe substantially homologous to a first portion of a nucleic acid encoding CPY1A1, wherein said first capture probe is directly adjacent to or includes at its terminus a detection position;

ii) at least one second capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY1A2, wherein said second capture probe is directly adjacent to or includes at its terminus a detection position;

iii) at least one third capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY1B1, wherein said third capture probe is directly adjacent to or includes at its terminus a detection position;

iv) at least one fourth capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY2C19, wherein said fourth capture probe is directly adjacent to or includes at its terminus a detection position;

v) at least one fifth capture probe substantially homologous to a first

portion of the sense strand of a nucleic acid encoding CPY2D6, wherein said fifth capture probe is directly adjacent to or includes at its terminus a detection position;

vi) at least one sixth capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY2E1, wherein said sixth capture probe is directly adjacent to or includes at its terminus a detection position; and

vii) at least one seventh capture probe substantially homologous to a first portion of the sense strand of a nucleic acid encoding CPY3A4, wherein said seventh capture probe is directly adjacent to or includes at its terminus a detection position;

b) hybridizing at least one target sequence to its corresponding capture probe to form a hybridization complex;

c) adding a polymerase and at least one dNTP comprising a label, under conditions whereby if said dNTP is perfectly complementary to a detection position, said dNTP is added to a capture probe to form an extended probe;

d) determining the nucleotide at the interrogation position of said extended probe.

10. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing an array comprising:

i) a solid support with a first surface comprising a hydrogel layer comprising an array of capture probes;

b) hybridizing said target sequence to at least one of said capture probes to form a hybridization complex; and

c) determining the nucleotide at said detection position.

11. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a solid support with a first surface comprising at least one non self-extension probe wherein self-extension of said non self-extension probe does not occur in the absence

of said target and wherein, said non self-extension probe includes an interrogation nucleotide;

b) hybridizing said target sequence to said non self- extension probe to form a hybridization complex;

c) contacting said surface with:

i) an extension enzyme; and

ii) at least one chain terminating nucleotide comprising a hapten;

under conditions whereby if said chain terminating nucleotide is perfectly complementary to the base of the target sequence immediately adjacent to the 3' end of said non self- extension probe in the hybridization complex, said chain terminating nucleotide is added to said non self-extension probe to form a modified extension probe;

d) contacting said modified extension probe with the binding partner of said hapten, wherein said hapten is labeled; and

e) detecting the presence of said label to determine the nucleotide at said detection position.

12. A method according to claim 11 wherein said interrogation nucleotide in said non self-extension probe is within two bases of its 3' terminal end and wherein, said 3' terminal end nucleotide is non-complementary to a corresponding base when a self-hybridizing structure of said non self-extension probe is formed.

13. A method according to claim 12 wherein said interrogation nucleotide is the 3' terminal nucleotide.

14. A method according to claim 12 wherein said interrogation nucleotide is the penultimate 3' terminal nucleotide.

15. A method according to claim 11 wherein said non self- extension probe comprises at least two modified nucleotides.

16. A method according to claim 15 wherein said modified nucleotides are exo-cyclic amine modified bases.

17. A method according to claim 15 wherein said modified nucleotides are terminator bases.

18. A method according to claim 16 wherein said exo-cyclic amine modified bases are selected from a group consisting of 2-thio thymine, 2-amino adenine, amine modified cytosine and amine modified guanine.

19. A method according to claim 17 wherein said terminator base is 4-methylindole .

20. A method according to claim 15 wherein said modified nucleotides alter protein binding and are present in the stem region of said non self-extension probe.

21. A method according to claim 20 wherein said modified nucleotide comprises a sugar modification.

22. A method according to claim 20 wherein said modified nucleotide comprises a phosphate modification.

23. A method according to claim 22 wherein said phosphate modifications are selected from a group consisting of phosphorothioates, phosphoramidates, methyl phosphonates, methyl phosphates, H-phosphonates.

24. A method according to claim 11 wherein self-extension of said non self-extension probe is inhibited by short complementary oligonucleotides.

25. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) amplifying the target DNA using random primers to generate DNA amplicons;

b) transcribing said DNA amplicons to generate RNA target sequences (*in vitro* transcription);

c) providing a solid support with a first surface comprising at least one extension probe wherein said extension probe includes an interrogation nucleotide;

b) hybridizing said RNA target sequence to said extension probe to form a hybridization complex;

c) contacting said surface with:

i) a modified reverse transcriptase; and

ii) at least one chain terminating nucleotide comprising a hapten;

under conditions whereby if said chain terminating nucleotide is perfectly complementary to the base of the target sequence immediately adjacent to the 3' end of said non self- extension probe in the hybridization complex, said chain terminating nucleotide is added to said non self- extension probe to form a modified extension probe;

d) contacting said modified extension probe with the binding partner of said hapten, wherein said binding partner is labeled; and

e) detecting the presence of said label to determine the nucleotide at said detection position.

26. A method according to claim 25 wherein said modified reverse transcriptase only extends extension probes bound to RNA.

27. A method according to claim 11 or 25 wherein said hapten is biotin.

28. A method according to claim 11 or 25 wherein said binding partner is streptavidin.

29. A method according to claim 11 or 25 wherein said binding partner is Alexa dye labeled streptavidin.

30. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) providing a solid support with a first surface comprising a solid support with a first surface comprising a hydrogel layer comprising at least one non self-extension probe, wherein self-extension said non self-extension probe does not occur in the absence of said target and wherein, said non self-extension probe includes an interrogation nucleotide;

b) hybridizing said target sequence to said non self-extension probe to form a hybridization complex;

c) contacting said surface with:

i) an extension enzyme; and

ii) at least one chain terminating nucleotide comprising a hapten;

under conditions whereby if said chain terminating nucleotide is perfectly complementary to the base of the target sequence immediately adjacent to the 3' end of said non self-extension probe in the hybridization complex, said chain terminating nucleotide is added to said non self-extension probe to form a modified extension probe;

d) contacting said modified extension probe with the binding partner of said hapten, wherein said binding partner is labeled; and

e) detecting the presence of said label to determine the nucleotide at said detection position.

31. A method according to claim 30 wherein said interrogation nucleotide in said non self-extension probe is within two bases of its 3' terminal end and wherein, said 3' terminal end nucleotide is non-complementary to a corresponding base when a self-hybridizing structure of said non self-extension probe is formed.

32. A method according to claim 31 wherein said interrogation nucleotide is the 3' terminal nucleotide.

33. A method according to claim 31 wherein said interrogation nucleotide is the penultimate 3' terminal nucleotide.

34. A method according to claim 30 wherein said non self- extension probe comprises at least two modified nucleotides.

35. A method according to claim 34 wherein said modified nucleotides are exo-cyclic amine modified bases.

36. A method according to claim 34 wherein said modified nucleotides are terminator bases.

37. A method according to claim 35 wherein said exo-cyclic amine modified bases are selected from a group consisting of 2-thio thymine, 2-amino adenine, amine modified cytosine and amine modified guanine.

38. A method according to claim 36 wherein said terminator base is 4-methylindole .

39. A method according to claim 34 wherein said modified nucleotides alter protein binding and are present in the stem region of said non self-extension probe.

40. A method according to claim 39 wherein said modified nucleotide comprises a sugar modification.

41. A method according to claim 39 wherein said modified nucleotide comprises a phosphate modification.

42. A method according to claim 41 wherein said phosphate modifications are selected from a group consisting of phosphorothioates, phosphoramidates, methyl phosphonates, methyl phosphates, H-phosphonates.

43. A method according to claim 30 wherein self-extension of said non self-extension probe is inhibited by short complementary oligonucleotides.

44. A method of determining the identification of a nucleotide at a detection position in a target sequence comprising:

a) amplifying the target DNA using random primers to generate DNA amplicons;

b) transcribing said DNA amplicons to generate RNA target sequences (*in vitro* transcription);

c) providing a solid support with a first surface comprising at least one extension probe wherein said extension probe includes an interrogation nucleotide;

b) hybridizing said RNA target sequence to said extension probe to form a hybridization complex;

c) contacting said surface with:

i) a modified reverse transcriptase; and

ii) at least one chain terminating nucleotide comprising a hapten;

under conditions whereby if said chain terminating nucleotide is perfectly complementary to the base of the target sequence immediately adjacent to the 3' end of said non self- extension probe in the hybridization complex, said chain terminating nucleotide is added to said non self- extension probe to form a modified extension probe;

d) contacting said modified extension probe with the binding partner of said hapten, wherein said binding partner is labeled; and

e) detecting the presence of said label to determine the nucleotide at said detection position.

45. A method according to claim 44 wherein said modified reverse transcriptase only extends extension probes bound to RNA.

46. A method according to claim 30 or 44 wherein said hapten is biotin.

47. A method according to claim 30 or 44 wherein said binding partner is streptavidin.

48. A method according to claim 30 or 44 wherein said binding partner is Alexa dye labeled

streptavidin.

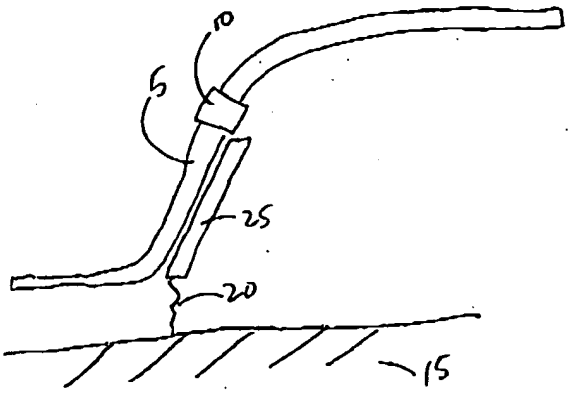

Fig 1A

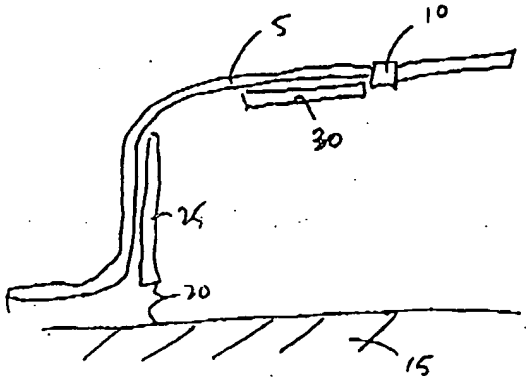

Fig 1B

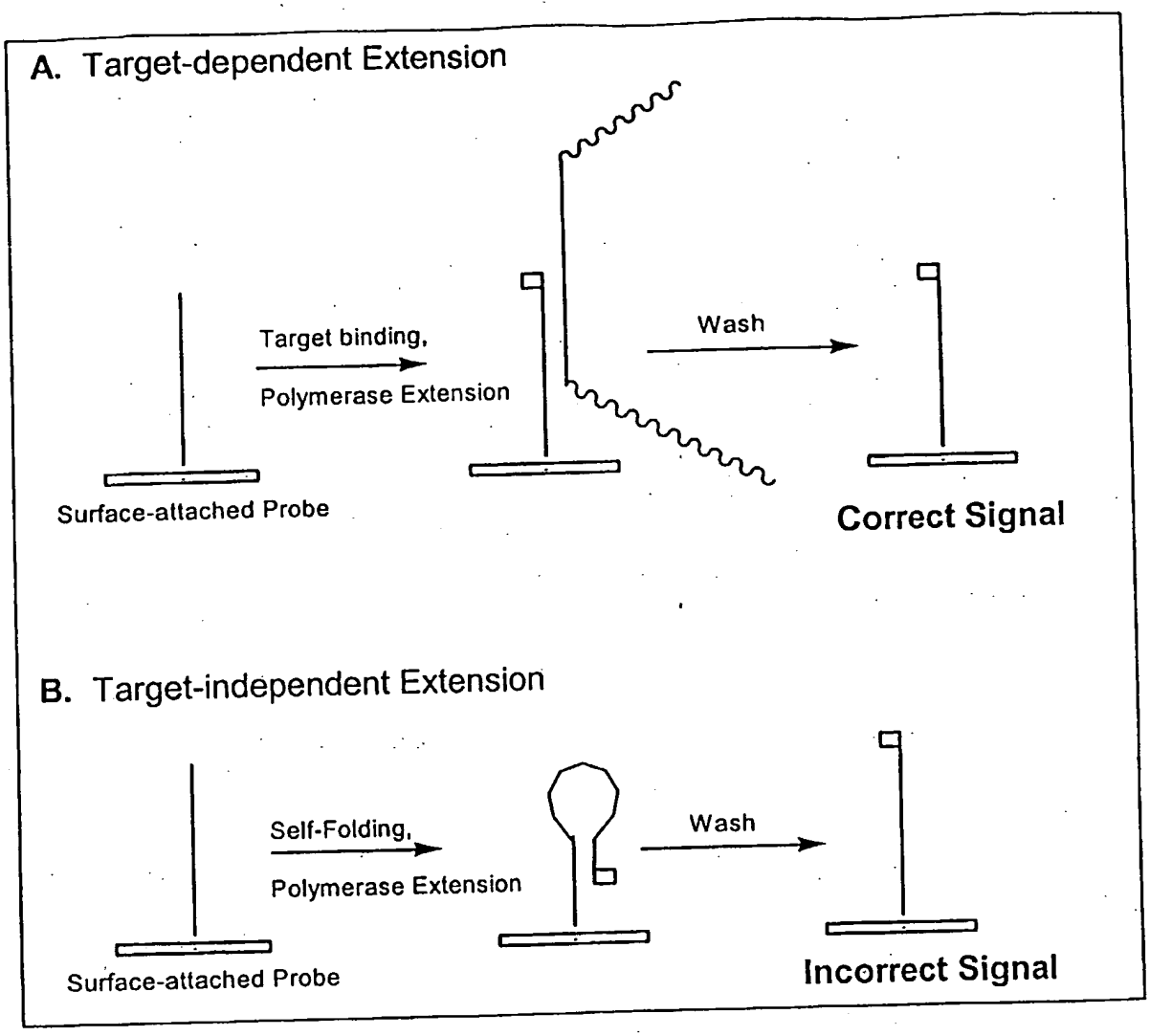
A. Target-dependent Extension
Target binding,
Polymerase Extension
Wash
Surface-attached Probe
Correct Signal
B. Target-independent Extension
Self-Folding,
Polymerase Extension
Wash
Surface-attached Probe
Incorrect Signal

Fig 3A

P450 SNP CHARACTERIZATION LIST

SNP ID	GENE	POSITION	FROM TRANSLATION START	SEQ SOURCE	EXON/INTRON LOCATION	MUTATION	CONSEQUENCE	ENZYME EFFECT (IN VIVO)
2D6 1618	CYP 2D6	1618	-1	GB [M33388]	5' FLANK		N/A	
2D6 1638	CYP 2D6	1638	19	GB [M33388]	EXON 1	G>A	V7M	
2D6 1650	CYP 2D6	1650	31	GB [M33388]	EXON 1	G>A	V11M	
2D6 1696	CYP 2D6	1696	77	GB [M33388]	EXON 1	G>A	R28H	
2D6 1701	CYP 2D6	1701	82	GB [M33388]	EXON 1	C>T	R29C	
2D6 1719	CYP 2D6	1719	100	GB [M33388]	EXON 1	C>T	P34S	
2D6 1743	CYP 2D6	1743	124	GB [M33388]	EXON 1	G>A	G42R	
2D6 1757	CYP 2D6	1757	138	GB [M33388]	EXON 1	InsT	FRAMESHIFT	NO ACTIVITY
2D6 2502	CYP 2D6	2502	883	GB [M33388]	INTRON 1	G>C	SPLICE DEFECT	
2D6 2576	CYP 2D6	2576	957	GB [M33388]	EXON 2	C>T	A85V	
2D6 2580	CYP 2D6	2580	974	GB [M33388]	EXON 2	C>A	L91M	
2D6 2603	CYP 2D6	2603	984	GB [M33388]	EXON 2	A>G	H94R	
2D6 2616	CYP 2D6	2616	997	GB [M33388]	EXON 2	C>G	SILENT	
2D6 2642	CYP 2D6	2642	1023	GB [M33388]	EXON 2	C>T	T107I	
2D6 2658	CYP 2D6	2658	1039	GB [M33388]	EXON 2	C>T	SILENT	
2D6 3278	CYP 2D6	3278	1659	GB [M33388]	EXON 3	G>A	V136M	
2D6 3280	CYP 2D6	3280	1661	GB [M33388]	EXON 3	G>C	SILENT	
2D6 3320	CYP 2D6	3320	1704	GB [M33388]	EXON 3	C>G	Q151E	
2D6 3326	CYP 2D6	3326	1707	GB [M33388]	EXON 3	T>del	FRAMESHIFT	NO ACTIVITY
2D6 3343	CYP 2D6	3343	1724	GB [M33388]	EXON 3	C>T	SILENT	
2D6 3368	CYP 2D6	3368	1748	GB [M33388]	EXON 3	A>G	N166D	
2D6 3377	CYP 2D6	3377	1758	GB [M33388]	EXON 3	G>T	G169 STOP	
2D6 3485	CYP 2D6	3485	1846	GB [M33388]	EXON 4	G>A	SPLICE DEFECT	
2D6 3477	CYP 2D6	3477	1858	GB [M33388]	EXON 4	C>T	R143C	
2D6 3488	CYP 2D6	3488	1869	GB [M33388]	EXON 4	T>C		
2D6 3562	CYP 2D6	3562	1949	GB [M33388]	EXON 4	G>A	R201H	
2D6 3582	CYP 2D6	3582	1978	GB [M33388]	EXON 4	InsG	FRAMESHIFT ?	
2D6 3585	CYP 2D6	3585	1976	GB [M33388]	EXON 4	G>A	G212E	
2D6 3597	CYP 2D6	3597	1978	GB [M33388]	EXON 4	C>T	SILENT	NORMAL
2D6 3598	CYP 2D6	3598	1979	GB [M33388]	EXON 4	T>C		
2D6 4089	CYP 2D6	4089	2470	GB [M33388]	EXON 5	T>C	SILENT	
2D6 4099	CYP 2D6	4099	2480	GB [M33388]	EXON 5	C>T	SILENT	
2D6 4102	CYP 2D6	4102	2483	GB [M33388]	EXON 5	G>T	A237S	NORMAL
2D6 4158	CYP 2D6	4158	2549	GB [M33388]	EXON 5	A>del	FRAMESHIFT	NO ACTIVITY
2D6 4184	CYP 2D6	4184	2575	GB [M33388]	EXON 5	C>A	SILENT	
2D6 4206	CYP 2D6	4206	2587	GB [M33388]	EXON 5	GACT>del	FRAMESHIFT	NO ACTIVITY
2D6 4232	CYP 2D6	4232	2613	GB [M33388]	EXON 5	AGA>del	K281 DEL	DECREASED
2D6 4469	CYP 2D6	4469	2850	GB [M33388]	EXON 6	C>T	R296C	
2D6 4472	CYP 2D6	4472	2853	GB [M33388]	EXON 6	A>C	I297L	
2D6 4554	CYP 2D6	4554	2935	GB [M33388]	EXON 6	A>C	H324P	NONE
2D6 4557	CYP 2D6	4557	2938	GB [M33388]	EXON 6	C>T	P325L	
2D6 4558	CYP 2D6	4558	2939	GB [M33388]	EXON 6	G>A	SILENT	
2D6 4802	CYP 2D6	4802	3183	GB [M33388]	EXON 7	G>A	V808M	
2D6 4817	CYP 2D6	4817	3198	GB [M33388]	EXON 7	C>G	R343G	
2D6 4898	CYP 2D6	4898	3277	GB [M33388]	EXON 7	T>C	I309T	
2D6 4907	CYP 2D6	4907	3286	GB [M33388]	EXON 7	G>A	G373S	
2D6 5447	CYP 2D6	5447	3828	GB [M33388]	EXON 8	G>A	SILENT	NORMAL
2D6 5472	CYP 2D6	5472	3853	GB [M33388]	EXON 8	G>A	E410K	
2D6 5496	CYP 2D6	5496	3877	GB [M33388]	EXON 8	G>C	E418Q	
2D6 5506	CYP 2D6	5506	3887	GB [M33388]	EXON 8	T>C		
2D6 5661	CYP 2D6	5661	4042	GB [M33388]	EXON 9	G>A	R440H	
2D6 5734	CYP 2D6	5734	4115	GB [M33388]	EXON 9	C>T	SILENT	
2D6 5799	CYP 2D6	5799	4180	GB [M33388]	EXON 9	G>C	S486T	"2, *4
2E1 1532	CYP 2E1	1532	-1290	GB [J02843]	5' FLANK	G>C		
2E1 1827	CYP 2E1	1827	-1196	GB [J02843]	5' FLANK	G>C		
2E1 1772	CYP 2E1	1772	-1053	GB [J02843]	5' FLANK	C>T		
2E1 1800	CYP 2E1	1800	-1025	GB [J02843]	5' FLANK	T>C		
2E1 2019	CYP 2E1	2019	-806	GB [J02843]	5' FLANK	T>C		
2E1 2473	CYP 2E1	2473	-352	GB [J02843]	5' FLANK	A>C		
2E1 2492	CYP 2E1	2492	-333	GB [J02843]	5' FLANK	T>A		
2E1 2754	CYP 2E1	2754	-71	GB [J02843]	5' FLANK	G>T		
2E1 3104	CYP 2E1	3104	280	GB [J02843]	INTRON A	NONE		
2E1 3085	CYP 2E1	3085	261	GB [J02843]	INTRON A	NONE		
2E1 3956	CYP 2E1	3956	1132	GB [J02843]	EXON 2	G>A	R76H	REDUCED

Fig 3B

SNP ID	GENE	POSITION	FROM TRANSLATION START	SEQ SOURCE	EXON/INTRON LOCATION	MUTATION	CONSEQUENCE	ENZYME EFFECT
					EXON 4	G>A	V178I	NORMAL
2E1 7592	CYP 2E1	7592	4768	GB J02843	INTRON F	T>A		
2E1 10486	CYP 2E1	10486	7632	GB J02843	INTRON G	C>G	V389I	
2E1 12720	CYP 2E1	12720	9899	GB J02845	EXON 8	G>A		
2E1 12847	CYP 2E1	12847	10025	GB J02843	EXON 8	C>T		
2E1 12945	CYP 2E1	12945	10121	GB J02843	5'FLANK	A>G		
3A4 816	CYP 3A4	816	-392	GB D11131	5'FLANK	A>G		
3A4 818	CYP 3A4	818	-390	GB D11131	5'FLANK	G>A		
1A1 1213	CYP 1A1	1213	-3229	GB J04390	5'FLANK	C>T		
1A1 1223	CYP 1A1	1223	-3219	GB J04390	EXON 7	C>A	T461N	
1A1 6568	CYP 1A1	6568	2453	GB J04390	EXON 7	A>G	I462V	
1A1 6570	CYP 1A1	6570	2455	GB J04390	3'FLANK	T>C		
1A1 7320	CYP 1A1	7320	3205	GB J04390	3'FLANK/FLOATER	T>C		
1A1 7916	CYP 1A1	7916	3600	GB J04390	INTRON 1(not translated)	T>C	N/A	
1B1 3783	CYP 1B1	3783	-15	GB U56438	EXON 2	C>G	R48G	
1B1 3847	CYP 1B1	3847	142	GB U56438	EXON 2	G>C	W57C	
1B1 3976	CYP 1B1	3976	171	GB U56438	EXON 2	G>A	G61E	
1B1 3987	CYP 1B1	3987	182	GB U56438	EXON 2	T>C	L77P	GLAUCOMA
1B1 4035	CYP 1B1	4035	230	GB U56438	EXON 2	G>T	A119S	
1B1 4160	CYP 1B1	4160	355	GB U56438	EXON 2	InsT	FRAMESHIFT	
1B1 4906	CYP 1B1	4906	501	GB U56439	EXON 2	G>T	E281X	
1B1 4946	CYP 1B1	4946	841	GB U56439	EXON 2	InsC	FRAMESHIFT	
1B1 4958	CYP 1B1	4958	853	GB U56438	EXON 2	C>T	G365W	
1B1 7930	CYP 1B1	7930	4125	GB U56439	EXON 3	G>A	R368H	GLAUCOMA
1B1 7940	CYP 1B1	7940	4135	GB U56439	EXON 3	G>A	D374N	GLAUCOMA
1B1 7957	CYP 1B1	7957	4152	GB U56438	EXON 3	C>T	P378L	
1B1 7973	CYP 1B1	7973	4168	GB U56439	EXON 3	G>A	E387K	
1B1 7996	CYP 1B1	7996	4191	GB U56439	EXON 3	G>A	R390H	
1B1 8006	CYP 1B1	8006	4201	GB U56438	EXON 3	C>G	L432V	
1B1 8131	CYP 1B1	8131	4326	GB U56439	EXON 3	C>T	P437L	
1B1 8147	CYP 1B1	8147	4342	GB U56439	EXON 3	T>C	449 SILENT	
1B1 8164	CYP 1B1	8164	4379	GB U56438	EXON 3	A>G	N453V	
1B1 8195	CYP 1B1	8195	4390	GB U56439	EXON 3	C>T	R469W	
1B1 8242	CYP 1B1	8242	4457	GB U56439	EXON 3	C>G		
1B1 8567	CYP 1B1	8567	4782	GB U56439	EXON 3	T>A		
1B1 8807	CYP 1B1	8807	5002	GB U56438	EXON 3	T>G		
1B1 9164	CYP 1B1	9164	5359	GB U56438	3'FLANK	C>A		HIGHER INDUCIBILITY
1A2 2640	CYP 1A2	2640	-164	GB M31664	INTRON A (5'FLANK)	C>G	F21L	
1A2 2665	CYP 1A2	2665	63	GB M31664	EXON 1	C>T		
2C19 69	CYP 2C19	69	69	GB NM 000769	EXON 1	G>C	E92D	
2C19 276	CYP 2C19	276	276	GB NM 000769	EXON 2	G>A	R132Q	
2C19 395	CYP 2C19	395	395	GB NM 000769	EXON 3	C>T		
2C19 430	CYP 2C19	430	430	GB NM 000769	EXON 3	G>A	STOP CODON	
2C19 636	CYP 2C19	636	636	GB NM 000769	EXON 4	G>A	SPLICE DEFECT	
2C19 681	CYP 2C19	681	681	GB NM 000769	EXON 5	G>A		

Fig 3C

ALLELE/HAPLOTYPE FAM	IUPAC CODE	ALLELE 1	ALLELE 2	SNP SOURCE INFO
				Error Corrections
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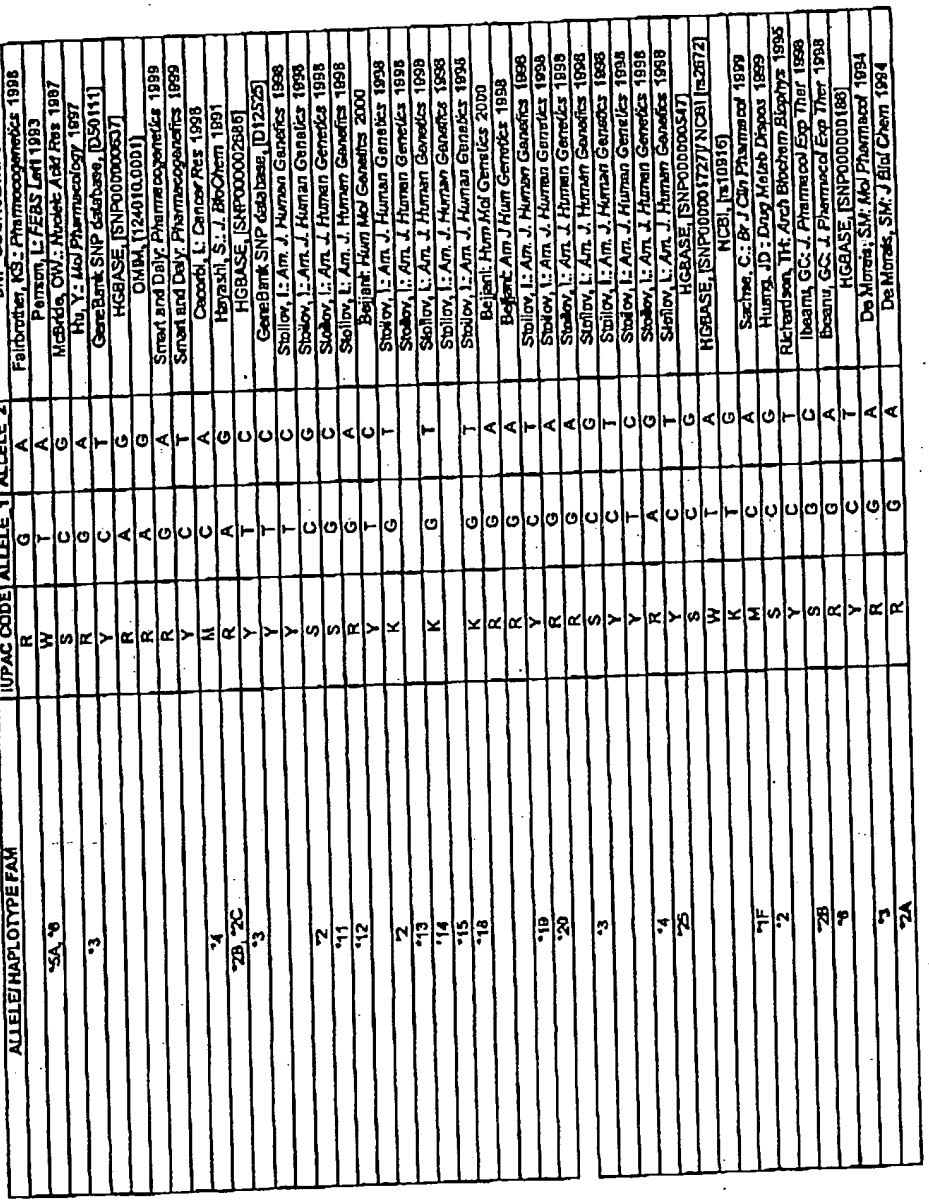
*35	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*21	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*22	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*4, *10 (*36), *14, *37	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*12	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*15			T	Sachse C.: *Pharmacogenetics* 1998
*11	S	G	C	Marez, D.: *Pharmacogenetics* 1997
*23	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*4	M	C	A	Marez, D.: *Pharmacogenetics* 1997
*4	R	A	G	Marez, D.: *Pharmacogenetics* 1997
*2, *4	S	C	G	Marez, D.: *Pharmacogenetics* 1997
*17	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*2, *4, *10 (*36), *37	Y	C	T	Marez, D.: *Pharmacogenetics* 1997.
*29	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*2, *4, *8, *10 (*36), *11, *12, *19, *28, *29, *30, *31, *32, *35, *37	S	G	C	Marez, D.: *Pharmacogenetics* 1997
*23	S	C	G	Marez, D.: *Pharmacogenetics* 1997
*8		T	DEL	Marez, D.: *Pharmacogenetics* 1997
*2	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*3	R	A	G	Marez, D.: *Pharmacogenetics* 1997
*8, *14	K	G	T	Marez, D.: *Pharmacogenetics* 1997
*4	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*4	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*1	Y	T	C	Sachse C.: *Pharmacogenetics* 1998
*37	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*20		INS	G	Marez-Allorge D.: *Pharmacogenetics* 1999
*6	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*1, *20	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*20	Y	T	C	Marez-Allorge D.: *Pharmacogenetics* 1999
*2	Y	T	C	Marez, D.: *Pharmacogenetics* 1997
	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*33	K	G	T	Marez, D.: *Pharmacogenetics* 1997
*3		A	DEL	Marez, D.: *Pharmacogenetics* 1997
*1, *2	M	C	A	Marez, D.: *Pharmacogenetics* 1997
*38		GACT	DEL	Leathart JB.: *Pharmacogenetics* 1998
*9		AGA	DEL	Marez, D.: *Pharmacogenetics* 1997
*2, *4, *8, *11, *12, *14, *17, *19, *20, *28, *29, *30, *31, *32, *34, *35	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*24	M	A	C	Marez, D.: *Pharmacogenetics* 1997
*7	M	A	C	Marez, D.: *Pharmacogenetics* 1997
*4	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*2	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*29	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*25	S	C	G	Marez, D.: *Pharmacogenetics* 1997
*28	Y	T	C	Marez, D.: *Pharmacogenetics* 1997
*6	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*1	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*27, *32	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*4	S	G	C	Marez, D.: *Pharmacogenetics* 1997
*4	Y	T	C	Yokota, H.: *Pharmacogenetics* 1993
*31	R	G	A	Marez, D.: *Pharmacogenetics* 1997
*2	Y	C	T	Marez, D.: *Pharmacogenetics* 1997
*6, *8, *10 (*36), *11, *12, *14, *17, *19, *20, *28, *29, *30, *31, *32, *	S	G	C	Marez, D.: *Pharmacogenetics* 1997
*5A, *5B	S	G	C	Hayashi, S.: *J. BioChem* 1991
	S	G	C	Hayashi, S.: *J. BioChem* 1991
*3A, *3B	Y	C	T	Hayashi, S.: *J. BioChem* 1991
	Y	T	C	Hayashi, S.: *J. BioChem* 1991
	Y	T	C	Hayashi, S.: *J. BioChem* 1991
	R	A	G	Fairbrother, KS.: *Pharmacogenetics* 1998
*7C	W	T	A	Fairbrother, KS.: *Pharmacogenetics* 1998
*7ALL	K	G	T	Fairbrother, KS.: *Pharmacogenetics* 1998
	G	G		Error Corrections
	T	T		Error Corrections
*2	R	G	A	Hu, Y.: *Mol Pharmacology* 1997

Fig. 3D



ALLELE/ HAPLOTYPE FAM	IUPAC CODE	ALLELE 1	ALLELE 2	SNP SOURCE INFO
	R	G	A	Fairbrother, KS.: *Pharmacogenetics* 1998
	W	T	A	Peterson, L.: *FEBS Lett* 1993
*5A, *6	S	C	G	McBride, OW.: *Nucleic Acid Res* 1987
	R	G	A	Hu, Y.: *Mol Pharmacology* 1997
*3	Y	C	T	GeneBank SNP database, [D30111]
	R	A	G	HGBASE [SNP00000037]
	R	A	G	OMIM [124010.0001]
	R	G	A	Smart and Daly: *Pharmacogenetics* 1999
	Y	C	T	Smart and Daly: *Pharmacogenetics* 1999
	M	C	A	Cascorbi, I.: *Cancer Res* 1998
*4	R	A	G	Hayashi, S.: *J. BioChem* 1991
*2B, *2C	R	A	C	HGBASE, [SNP00002886]
*3	Y	T	C	GeneBank SNP database, [D12525]
	Y	T	C	Stoilov, I.: *Am. J. Human Genetics* 1998
	Y	T	C	Stoilov, I.: *Am. J. Human Genetics* 1998
	S	C	G	Stoilov, I.: *Am. J. Human Genetics* 1998
*2	S	G	C	Stoilov, I.: *Am. J. Human Genetics* 1998
*11	R	G	A	Stoilov, I.: *Am. J. Human Genetics* 1998
*12	R	G	A	Beilant: *Hum Mol Genetics* 2000
	Y	T	C	Stoilov, I.: *Am. J. Human Genetics* 1998
	K	G	T	Stoilov, I.: *Am. J. Human Genetics* 1998
*2				Stoilov, I.: *Am. J. Human Genetics* 1998
*13	K	G	T	Stoilov, I.: *Am. J. Human Genetics* 1998
*14				Stoilov, I.: *Am. J. Human Genetics* 1998
*15	K	G	T	Stoilov, I.: *Am. J. Human Genetics* 1998
*18	K	G	A	Beilant: *Hum Mol Genetics* 2000
	R	G	A	Beilant: *Am J Hum Genetics* 1998
	R	G	A	Stoilov, I.: *Am. J. Human Genetics* 1998
*19	Y	C	T	Stoilov, I.: *Am. J. Human Genetics* 1998
*20	R	G	A	Stoilov, I.: *Am. J. Human Genetics* 1998
	R	G	A	Stoilov, I.: *Am. J. Human Genetics* 1998
	S	C	G	Stoilov, I.: *Am. J. Human Genetics* 1998
*3	S	C	G	Stoilov, I.: *Am. J. Human Genetics* 1998
	Y	C	T	Stoilov, I.: *Am. J. Human Genetics* 1998
	Y	T	C	Stoilov, I.: *Am. J. Human Genetics* 1998
	R	A	G	Stoilov, I.: *Am. J. Human Genetics* 1998
*4	R	C	G	Stoilov, I.: *Am. J. Human Genetics* 1998
*25	Y	C	T	HGBASE, [SNP00000547]
	S	C	G	HGBASE, [SNP00001727] [NCBI [m2672]
	W	T	A	NCBI, [hs10916]
	K	T	G	Sachse, C.: *Br J Clin Pharmacol* 1999
	M	C	A	Huang, JD.: *Drug Metab Dispos* 1999
*1F	S	C	G	Richardson, TH.: *Arch Biochem Biophys* 1995
*2	Y	C	T	Ibeanu, GC.: *J. Pharmacol Exp Ther* 1998
	S	G	C	Ibeanu, GC.: *J. Pharmacol Exp Ther* 1998
*2B	R	G	A	HGBASE, [SNP00000188]
*6	Y	C	T	De Morais, SM.: *Mol Pharmacol* 1994
	R	G	A	De Morais, SM.: *J Biol Chem* 1994
*3	R	G	A	
*2A				

CYP2D6 and its pseudogenes: similarity by region

S. Kimura et al. *Am J Hum Genet* (1989) 45:889-904

Fig 4

	Length, bp			Similarity, %		
	CYP2D6	CYP2D7	CYP2D8	D6/D7	D7/D8	D6/D8
UPSTREAM	774	777	265	97		
		186	183		92	
	189		186			89
EXON 1	268	269	265	97	94	93
INTRON 1	703	701	1620*	98	90	89
EXON 2	172	172	172	95	94	91
INTRON 2	550	528	546	74	78	77
EXON 3	153	153	153	98	93	92
INTRON 3	88	88	88	98	91	93
EXON 4	161	161	161	98	89	91
INTRON 4	433	425	449	94	85	86
EXON 5	177	177	177	99	93	92
INTRON 5	190	192	186	97	84	83
EXON 6	142	142	142	94	92	96
INTRON 6	207	194	204	82	87	90
EXON 7	188	188	185	98	94	95
INTRON 7	454	454	449	98	91	91
EXON 8	142	142	142	99	96	96
INTRON 8	98	98	96	100	97	97
EXON 9	252	252		94		
3'-FLANKING		180	181		95	
	180		181			92
	538	528		97		

* 3 *Alu* repeats insertion

Fig 5

P450 PRIMER LIST 02/22/01

GENE SEQ ID	START POSITION	DIRECTION	SEQ SOURCE	EXON/INTRON LOCATION	SEQUENCE	PRIMER LENGTH	Tm	BLAST RESULTS
CYP 2D6	1278	FORWARD	GB [M33388]	5' FLANK	CCCAGAAGGCTTTGCAGGCTTCA	23	71	ACCEPTABLE
CYP 2D6	6799	REVERSE	GB [M33388]	EXON 9	CTCACCAGGAAAGCAAAGACACCAT	25	67	ACCEPTABLE
CYP 2E1	1487	FORWARD	GB [J02843]	5' FLANK	TGAAGCCTCTGCCAGAGGCCAA	22	71	ACCEPTABLE
CYP 2E1	4022	REVERSE	GB [J02843]	EXON 2	GAGAACTCGTCCTTGTAGTCCAGCA	25	65	ACCEPTABLE
CYP 2E1	7445	FORWARD	GB [J02843]	INTRON 3	CACCTTCTCACAGGCCTTGGTGAA	24	69	ACCEPTABLE
CYP 2E1	10589	REVERSE	GB [J02843]	INTRON 6	CACCCTGTGCCTCTGAGGTTGAA	23	68	ACCEPTABLE
CYP 2E1	12667	FORWARD	GB [J02843]	INTRON 8	CCTGACCCCTGACTGCTTTCTATCTAA	27	68	ACCEPTABLE
CYP 2E1	13030	REVERSE	GB [J02843]	INTRON 8	AGGAGTGTGGGCTGCTCCTCAA	22	68	ACCEPTABLE
CYP 3A4	747	FORWARD	GB [D11131]	5' FLANK	CTGTAGGTGTGGCTTGTTGGCATGAA	26	69	ACCEPTABLE
CYP 3A4	941	REVERSE	GB [D11131]	5' FLANK	CACACCACTCACTGACCTCCTTTGA	25	67	ACCEPTABLE
CYP 1A1	7080	FORWARD	GB [X04300]	EXON 7	CTCTGGTTACAGGAAGCTATGCGTCAA	27	67	ACCEPTABLE
CYP 1A1	8206	REVERSE	GB [X04300]	3' FLANK	CATGCAAGCTCAATGCAGGCTAGAATAGAA	30	70	ACCEPTABLE
CYP 1B1	3698	FORWARD	GB [U56438]	INTRON 1	CTCTCCACCCAACGGCACTCA	21	68	ACCEPTABLE
CYP 1B1	4704	REVERSE	GB [U56438]	EXON 2	GCAGAGAGGATAAAGGCGTCCATCA	25	69	ACCEPTABLE
CYP 1B1	7883	FORWARD	GB [U56436]	EXON 3	ATCCTGATGTGCAGACTCCGAGTGCA	25	70	ACCEPTABLE
CYP 1B1	9235	REVERSE	GB [U56438]	EXON 3	CAAGCAAAGAGGTACAACATCACCTTGGA	30	70	ACCEPTABLE
CYP 1A2	2595	FORWARD	GB [M31664]	5' FLANK	CCAGCTCTCAGATTCTGTGATGCTCAA	27	69	ACCEPTABLE
CYP 1A2	2972	REVERSE	GB [M31664]	EXON 1	GGGTCAGCACATGCCCGAGCAA	22	74	ACCEPTABLE
CYP 2C19	197	FORWARD	GB [NM_000769]	EXON 2	CTCTGTATTATGGCCTGGAAGCATG	26	70	ACCEPTABLE
CYP 2C19	787	REVERSE	GB [NM_000769]	EXON 5	TCCCGAGGCTTGTTGATGTCCATC	24	70	ACCEPTABLE

PROBE ID	SEQUENCE
CYP1A1_V_2_70.6568.A.S	GCAAGCGGAAGTGTATCGGTGAGAA
CYP1A1_V_2_70.6568.C.S	GCAAGCGGAAGTGTATCGGTGAGAC
CYP1A1_60.6570.A.A	TCCCAGCGGGCAAT
CYP1A1_60.6570.G.A	TCCCAGCGGGCAAC
CYP1A1_V_2_60.7320.C.A	ATAAGGGTCTTACAAGGCCG
CYP1A1_V_2_60.7320.T.A	AATAAGGGTCTTACAAGGCCA
CYP1A2_60+1.2640.A.A	CATCTACCATGCGTCCTGTG
CYP1A2_60+1.2640.C.A	ATCTACCATGCGTCCTGGG
CYP1A2_V2.2866.C.S	TGGCCTCTGCCATCTTCT
CYP1A2_V2.2866.G.S	TGGCCTCTGCCATCTTG
CYP1A2_V3.2866.C.S	TGGCCTCTGCCATCTTCT
CYP1A2_V3.2866.G.S	TGGCCTCTGCCATCTTGT
CYP1B1_60.3793.C.A	CCATGCTGGGGACAGAG
CYP1B1_60.3793.T.A	CCATGCTGGGGACAGAA
CYP1B1_60.3947.C.S	GAGGCGGCAGCTCC
CYP1B1_60.3947.G.S	GAGGCGGCAGCTCG
CYP1B1_60.3976.C.S	GCCCGTTTGCGTGC
CYP1B1_60.3976.G.S	GCCCGTTTGCGTGG
CYP1B1_60.3987.A.A	GCCGCCGCGTTTT
CYP1B1_60.3987.G.A	GCCGCCGCGTTTC
1B1_4035.C.S	CGTTCGCTCGCCC
1B1_4035.T.S	CTCGTTCGCTCGCCT
CYP1B1_60+2-1.4160.G.A	GAAGGAGGCGAAGGCCG
CYP1B1_60+2-1.4160.T.A	GAAGGAGGCGAAGGACG
1B1_V2.4306.A.A	TCAGCACGTGGCCCT
1B1_V2.4306.T.A	CAGCACGTGGCCCAG
CYP1B1_60+1.4646.G.S	AGTTCTTGAGGCACTGCGA
CYP1B1_60+1.4646.T.S	CAAGTTCTTGAGGCACTGCTA
1B1_4668.C.A	TCGCGGGGGGG
1B1_4668.G.A	TCGCGGGGGGC
CYP1B1_60.7930.G.S	GAATTGGATCAGGTCGTGG
CYP1B1_60.7930.T.S	AGAATTGGATCAGGTCGTGT
1B1_V2.7940.A.A	TGGTIACCCATACAAGGCAGAT
1B1_V2.7940.G.A	GGTIACCCATACAAGGCAGACG
CYP1B1_60+1.7957.A.S	CGTCTGCCTTGTATGGGTAA
CYP1B1_60+1.7957.G.S	CGTCTGCCTTGTATGGGTGA
CYP1B1_60.7973.C.A	GGAAGGCCAGGACATAGG
CYP1B1_60.7973.T.A	AGGAAGGCCAGGACATAGA
CYP1B1_60.7996.A.S	TATGTCCTGGCCTTCCTTTATA
CYP1B1_60.7996.G.S	GTCCTGGCCTTCCTTTATG
CYP1B1_60+1.8131.C.S	GTCTGTGAATCATGACCCACT
CYP1B1_60+1.8131.G.S	GTCTGTGAATCATGACCCAGT
CYP1B1_60+1°.8184.C.A	GTCCTTGITGATGAGGCCGT
CYP1B1_60+1°.8184.T.A	GTCCTTGITGATGAGGCCAT
CYP1B1_60.8195.A.A	TGCTGGTCAGGTCCTTGT
CYP1B1_60.8195.G.A	GCTGGTCAGGTCCTTGC
CYP1B1_60.8242.C.S	TTCAGTGGGCAAAAGGC
CYP1B1_60.8242.T.S	TTTTCAGTGGGCAAAAGGT
CYP1B1_60.8587.C.S	TCAATTAGCGTTTAAGGTGAGC
CYP1B1_60.8587.G.S	TCAATTAGCGTTTAAGGTGAGG
CYP1B1_60.8807.A.S	CCCAAACACTTACACCAAACA
CYP1B1_60.8807.T.S	ACCCAAACACTTACACCAAACT
CYP1B1_60+1.9164.G.S	GAGTATAGTGGGGTTCCATGAGT
CYP1B1_60+1.9164.T.S	GAGTATAGTGGGGTTCCATGATT
CYP2C19EXONS_70.276.C.A	GAAATGGCCTCTTCCAGAAAACTCG
CYP2C19EXONS_70.276.G.A	GGAAATGGCCTCTTCCAGAAAACTCC
CYP2C19EXONS_70.395.A.A	CTCCTCTTCCCCATCCCAAAATTCT
CYP2C19EXONS_70.395.G.A	CCTCTTCCCCATCCCAAAATTCC

Fig 6A

CYP2C19EXONS_70.430.T.A	AGCGGGCTTCCTCTTGAACACA
CYP2C19EXONS_60.636.A.S	GATTGTAAGCACCCCCTGA
CYP2C19EXONS_60.636.G.S	TTGTAAGCACCCCCTGG
CYP2C19EXONS_60.681.A.S	CCACTATCATTGATTATTTCCCA
CYP2C19EXONS_60.681.G.S	CCACTATCATTGATTATTTCCCG
CYP2D6_70.1698.A.S	AGGCAGITATGGGGCTAGAAGCACTGA
CYP2D6_70.1698.G.S	GGCAGITATGGGGCTAGAAGCACTGG
CYP2D6_70.1650.A.A	AGGAGCAGGAAGATGGCCACTATCAT
CYP2D6_70.1650.G.A	GGAGCAGGAAGATGGCCACTATCAC
CYP2D6_70.1696.A.S	GGACCTGATGCACCGGCA
CYP2D6_70.1696.G.S	GGACCTGATGCACCGGCG
CYP2D6_70.1701.C.A	TGIGTAGCGTGCAGCCCAGCG
CYP2D6_70.1701.T.A	GTGIGTAGCGTGCAGCCCAGCA
CYP2D6_60.1719.C.A	GGGGGCCTGGTGG
CYP2D6_60.1719.T.A	AGGGGGCCTGGTGA
CYP2D6_70.1743.A.S	CCCCCTGCCACTGCCCA
CYP2D6_70.1743.G.S	CCCCTGCCACTGCCCG
2D6H.1757.G.S	CCCTGCCACTGCCCIGGCTGGGCAACCTG
2D6H.1757.T.S	CCCTGCCACTGCCCIGGCTGGGCAACCTT
2D6H_V2.1757.G.S	CCTGCCACTGCCCIGGCTGGGCAACCTGCT
2D6H_V2.1757.T.S	CCTGCCACTGCCCIGGCTGGGCAACCTTCT
CYP2D6_60+1.2502.C.A	CGGCGCCGCAAGT
CYP2D6_60+1.2502.G.A	CGGCGCCGCAACT
CYP2D6_60+1.2502.C.S	TGACCCTCCCTCTGCACT
CYP2D6_60+1.2502.G.S	TGACCCTCCCTCTGCAGT
CYP2D6_60.2576.C.S	GCTCAATGGGCTGGC
CYP2D6_60.2576.T.S	GTGCTCAATGGGCTGGT
CYP2D6_60.2593.A.A	CGCCGIGGGTCACCAT
CYP2D6_60.2593.C.A	CGCCGIGGGTCACCAG
CYP2D6_70+*.2603.A.S	GAGGCGITGGTGACCCACG
CYP2D6_70+*.2603.G.S	CGAGGCGITGGTGACCCG
CYP2D6_60+2-1.2616.C.A	GCGGTCGGCGGT
CYP2D6_60+2-1.2616.G.A	GGCGGTCGGCCGT
CYP2D6_60+1.2642.C.S	GCCTGTGCCCATCACC
CYP2D6_60+1.2642.T.S	CGCCTGTGCCCATCATC
CYP2D6_60+2.2642.C.A	CCIAAACCCAGGATCTGGGTG
CYP2D6_60+2.2642.T.A	CCIAAACCCAGGATCTGGATG
CYP2D6_70+1.2658.C.A	TGGGAACGCGGCCCGA
CYP2D6_70+1.2658.T.A	TGGGAACGCGGCCCAA
CYP2D6_60+1.3278.A.S	CAGAGGCGCTTCTCCAT
CYP2D6_60+1.3278.G.S	CAGAGGCGCTTCTCCGT
CYP2D6_60.3280.C.S	CAGAGGCGCTTCTCCITC
CYP2D6_60.3280.G.S	CAGAGGCGCTTCTCCITG
CYP2D6_70+1.3323.C.S	TGGGCAAGAAGTCGCTGGAGCA
CYP2D6_70+1.3323.G.S	TGGGCAAGAAGTCGCTGGAGGA
2D6H.3326.G.A	GCIGCCTCCTCGGTCACCCC
2D6H.3326.T.A	GCIGCCTCCTCGGTCACCCA
2D6H_V2.3326.G.A	GCIGCCTCCTCGGTCACCCCT
2D6H_V2.3326.T.A	GCIGCCTCCTCGGTCACCCAC
CYP2D6_70.3343.C.A	CGGCACAAAGGCAGGCG
CYP2D6_70.3343.T.A	GCGGCACAAAGGCAGGCA
CYP2D6_70.3368.A.S	TGTGCCGCCTTCGCCA
CYP2D6_70.3368.G.S	GTGCCGCCTTCGCCG
CYP2D6_70.3377.G.S	CGCCTTCGCCIACCACTCCG
CYP2D6_70.3377.T.S	CCGCCTTCGCCIACCACTCCT
CYP2D6_60.3465.A.S	CATCTCCCACCCCCAA
CYP2D6_60.3465.G.S	CATCTCCCACCCCCAG
CYP2D6_60.3477.C.A	AGAGICCGTTGGGGCG
CYP2D6_60.3477.T.A	AAGAGICCGTTGGGGCA
CYP2D6_60.3488.C.A	CGGCTTTGTCCAAGAGG

Fig 6B

CYP2D6_60.3562.A.A	CCAGCAGCCTGAGGAAGT
CYP2D6_60.3562.G.A	CAGCAGCCTGAGGAAGC
2D6H.3592.A.S	TCAGGCTGCTGGACCTAGCTCAGGA
2D6H.3592.G.S	CAGGCTGCTGGACCTAGCTCAGGGA
CYP2D6_60.3595.A.S	TGGACCTAGCTCAGGAGGA
CYP2D6_60.3595.G.S	GGACCTAGCTCAGGAGGG
CYP2D6_70.3597.C.S	GCTGCTGGACCTAGCTCAGGAGGIAC
CYP2D6_70.3597.T.S	GCTGCTGGACCTAGCTCAGGAGGIAT
CYP2D6_60.3598.C.A	CCCGACTCCTCCTTCG
CYP2D6_60.3598.T.A	GCCCGACTCCTCCTTCA
CYP2D6_70.4099.C.S	TCCTCCTGCAIATCCCAGCGC
CYP2D6_70.4099.T.S	GTCCTCCTGCAIATCCCAGCGT
2D6H_V2.4168.A.S	CTGGATGAGCTGCTAACTGAGCACAGG
2D6H_V2.4168.G.S	CTGGATGAGCTGCTAACTGAGCACGGG
2D6H_V3.4168.A.S	GCTGGATGAGCTGCTAACTGAGCACA
2D6H_V3.4168.G.S	GCTGGATGAGCTGCTAACTGAGCACGG
CYP2D6_70.4194.A.S	GGGACCCAGCCCAGCCA
CYP2D6_70.4194.C.S	GGGACCCAGCCCAGCCC
2D6H.4206.G.S	GCCCAGCCICCCCGAGACCTGAGG
2D6H.4206.T.S	GCCCAGCCICCCCGAGACCTGACT
2D6H.4232.A.A	TGGCAGCCACTCTCACCTTCT
2D6H.4232.G.A	TGGCAGCCACTCTCACCTC
CYP2D6_60.4469.C.S	GCTTCAATGATGAGAACCTGC
CYP2D6_60.4469.T.S	AGCTTCAATGATGAGAACCTGT
CYP2D6_70.4472.A.A	GCAGAGAACAGGTCAGCCACCACTAT
CYP2D6_70.4472.C.A	GCAGAGAACAGGTCAGCCACCACTAG
CYP2D6_V3.4554.C.A	TGGGCTCACGCTGCACATCIIGAGG
CYP2D6_V3.4554.A.A	GCTCACGCTGCACATCIIGAT
CYP2D6_V2.4554.C.A	GCTCACGCTGCACATCIIGAGG
CYP2D6_V2.4554.A.A	GCTCACGCTGCACATCIIGAT
CYP2D6_70.4557.C.S	GGCCTCCTGCTCATGATCCTACITCC
CYP2D6_70.4557.T.S	GGGCCTCCTGCTCATGATCCTACITCT
CYP2D6_70.4558.A.A	TGGGCTCACGCTGCACATCT
CYP2D6_70.4558.G.A	GGGCTCACGCTGCACATCC
CYP2D6_70.4802.A.S	GTGTCCAACAGGAGATCGACGACA
CYP2D6_70.4802.G.S	TGTCCAACAGGAGATCGACGACG
CYP2D6_70+*.4817.C.S	TCGACGACITGATAGGGCAGGTGCGG
CYP2D6_70+*.4817.G.S	ATCGACGACITGATAGGGCAGGTGGG
CYP2D6_70.4896.C.S	TGCAGCGCTTTGGGGACAC
CYP2D6_70.4896.T.S	GTGCAGCGCTTTGGGGACAT
CYP2D6_60.4907.A.S	GGACAICGTCCCCCTGA
CYP2D6_60.4907.G.S	GGACAICGTCCCCCTGG
CYP2D6_70.5447.A.A	AGACGGCCTCATCCTTCAGCACT
CYP2D6_70.5447.G.A	ACGGCCTCATCCTTCAGCACC
CYP2D6_70.5472.A.S	CTGAAGGATGAGGCCGTCTGGA
CYP2D6_70.5472.G.S	TGAAGGATGAGGCCGTCTGGG
CYP2D6_70.5496.C.S	CCTTCCGCTTCCACCCCC
CYP2D6_70.5496.G.S	CCTTCCGCTTCCACCCCG
CYP2D6_70+1.5506.C.S	CGCTTCCACCCCIAACACTTCCCG
CYP2D6_70+1.5506.T.S	CCGCTTCCACCCCIAACACTTCCTG
CYP2D6_70+1.5661.A.S	CCCCTCCCCACAGGCCAC
CYP2D6_70+1.5661.G.S	CCCTCCCCACAGGCCGC
CYP2D6_70.5734.C.A	CAGTGGGCACCGAGAAGCTG
CYP2D6_70.5734.T.A	TCCAGTGGGCACCGAGAAGCTA
CYP2E1_60-1+1.1532.C.A	CTGCACCTAACACTGCAGC
CYP2E1_60-1+1.1532.G.A	CTGCACCTAACACTGCACC
CYP2E1_60.1627.C.A	CATTCTATACTTGTATTTATACAAAAATGAGAG
CYP2E1_60.1627.G.A	CATTCTATACTTGTATTTATACAAAAATGAGAC
CYP2E1_V2.1772.C.A	TCTTAATTCATAGGTTGCAATTTTGTA
CYP2E1_V2.1772.T.A	TTCTTAATTCATAGGTTGCAATTTTATA

Fig 6C

CYP2E1_V3.1800.T.S	TTGCAACCTATGAATTAAGAACTTCTA
CYP2E1_V3.1800.C.S	ATTGCAACCTATGAATTAAGAACTCC
CYP2E1_60+1.2019.C.A	GATTTGTTTTACATTAGGGTAAATTTGG
CYP2E1_60+1.2019.T.A	GGATTTGTTTTACATTAGGGTAAATTTAG
2E1_2492.A.A	GTGGGGTGAGGTACCGT
2E1_2492.T.A	GTGGGGTGAGGTACCGA
2E1_2492.A.S	TGCCAAAGGGCAGGA
2E1_2492.T.S	GTGCCAAAGGGCAGGT
2E1_2473.A.A	GCCCTTTGGCACTGGT
2E1_2473.G.A	CCCTTTGGCACTGGC
2E1_2473.A.S	GGAGTTCCCCGTTGTCTAA
2E1_2473.G.S	GGAGTTCCCCGTTGTCTAG
CYP2E1_60.2754.G.S	GGGTCACCCTCCTTCTCAG
CYP2E1_60.2754.T.S	GGGTCACCCTCCTTCTCAT
CYP2E1_60+2.3956.A.S	GTGGGCTCGCAGCACA
CYP2E1_60+2.3956.G.S	TGGGCTCGCAGCGCA
CYP2E1_V2.3956.A.A	CCGTGCATCACCACCATGT
CYP2E1_V2.3956.G.A	GTGCATCACCACCATGCG
CYP2E1_60.10456.A.S	CACACCCAGCTGATTAAAAATTA
CYP2E1_60.10456.T.S	CACACCCAGCTGATTAAAAATTT
CYP2E1_60.12720.C.S	TCACTAAGCAACTCCTTCAACTC
CYP2E1_60.12720.G.S	TCACTAAGCAACTCCTTCAACTG
CYP2E1_60.12847.A.S	TTTCTCCTAGGGCACAGTCA
CYP2E1_60.12847.G.S	TCTCCTAGGGCACAGTCG
CYP2E1_60.12945.C.A	GGCTTGAAATAGTCACTGTACTTG
CYP2E1_60.12945.T.A	AATGGCTTGAAATAGTCACTGTACTTA
CYP3A4_60.816.A.S	GCCATAGAGACAAGGGCAA
CYP3A4_60.816.G.S	GCCATAGAGACAAGGGCAG
CYP3A4_60.918.A.S	CCAGTAACATTGATTGAGTTGTTTA
CYP3A4_60.918.G.S	CAGTAACATTGATTGAGTTGTTTG
Amplicon Control Probes	
1A1.23F22R_A.X.A	GCAGGATCCCTTAGGCTTG
1A1.23F22R_B.X.S	AGCCAGGAGGCCTGCTA
1A2.5F3R_A.X.S	TATCCAGCTGGGAGCCAA
1A2.5F3R_B.X.S	CCAGCCCCATGGCTCT
1B1.2F4R_A.X.S	CACGACGACCCCGAGTT
1B1.2F4R_B.X.S	CGGTGCGCACCGTT
1B1.8F11R_A.X.A	TTGGGTTGGCCCTGAA
1B1.8F11R_B.X.S	TGGGCTATGCAGGAGCTT
2C19.3F6R_A.X.A	GCACAGCCCAGGATGAA
2C19.3F6R_B.X.A	CATGCAGCACCACCATG
2D6.1F1R_A.X.S	AGCCCATTTGGTAGTGAGGCAGG
2D6.1F1R_B.X.S	GAGCCCATTTGGTAGTGAGGCAGA
2E1.1F6R_A.X.A	AGGITGGTATTGAACAACCACAA
2E1.1F6R_B.X.A	ATTCAGGTAATTCACAACAGGC
2E1.8F19R_A.X.S	GACTGTGGCCGACCTGTT
2E1.8F19R_B.X.S	GCACAGTGCAGAGCGCTT
2E1.11F13R_A.X.S	CCAGATGAAAGCCCACATT
2E1.11F13R_B.X.S	AAGCCCACATTTTGTTAACATG
3A4.1F1R_A.X.S	GCTTGTTGGGATGAATTTCAA
3A4.1F1R_B.X.S	CTGATAAGAACCCAGAACCCTT

Fig 6D

Beta SNP Content List

Fig 7

1A1

					Comments
NONE	CYP 1A1	1213	CYP1A1_V_2_60.1213.A.S	CYP1A1_V_2_60.1213.G.S	No Amplicon Coverage
NONE	CYP 1A1	1223	CYP1A1_V_2_60.1223.C.A	CYP1A1_V_2_60.1223.T.A	No Amplicon Coverage
23F22R	CYP 1A1	6568	CYP1A1_V_2_70.6568.A.S	CYP1A1_V_2_70.6568.C.S	
23F22R	CYP 1A1	6570	CYP1A1_60.6570.A.A	CYP1A1_60.6570.G.A	
			CYP1A1_V_2_70.6570.A.A	CYP1A1_V_2_70.6570.G.A	Remove unneeded redundancy
23F22R	CYP 1A1	7320	CYP1A1_V_2_60.7320.C.A	CYP1A1_V_2_60.7320.T.A	
NONE	CYP 1A1	7547	CYP1A1_60+1.7547.A.S	CYP1A1_60+1.7547.T.S	No Amplicon Coverage
23F22R	CYP 1A1	CNTRL	1A1.23F22R_A.X.A		Independent Amplicon Controls
23F22R	CYP 1A1	CNTRL	1A1.23F22R_B.X.S		Independent Amplicon Controls

1A2

5F3R	CYP 1A2	2640	CYP1A2_60+1.2640.A.A	CYP1A2_60+1.2640.C.A	Redesign to overcome possible selfX
			CYP1A2_60+#.2640.A.A	CYP1A2_60+#.2640.C.A	Remove unneeded redundancy
5F3R	CYP 1A2	2866	CYP1A2_V2.2866.C.S	CYP1A2_V2.2866.G.S	Redesign of one Probe (CYP1A2_V2.2866.GS = CYP1A2_60.2866.G
			CYP1A2_V3.2866.C.S	CYP1A2_V3.2866.G.S	
5F3R	CYP 1A2	CNTRL	1A2.5F3R_A.X.S		Independent Amplicon Controls
5F3R	CYP 1A2	CNTRL	1A2.5F3R_B.X.S		Independent Amplicon Controls

1B1

2F4R	CYP 1B1	3793	CYP1B1_60.3793.C.A	CYP1B1_60.3793.T.A	
2F4R	CYP 1B1	3947	CYP1B1_60.3947.C.S	CYP1B1_60.3947.G.S	
2F4R	CYP 1B1	3976	CYP1B1_60.3976.C.S	CYP1B1_60.3976.G.S	
2F4R	CYP 1B1	3987	CYP1B1_60.3987.A.A	CYP1B1_60.3987.G.A	
2F4R	CYP 1B1	4035	1B1_4035.C.S	1B1_4035.T.S	Newly Identified SNP
2F4R	CYP 1B1	4160	CYP1B1_60+2-1.4160.G.A	CYP1B1_60+2-1.4160.T.A	Redesigned to overcome GG self extension
2F4R	CYP 1B1	4306	1B1_V2.4306.A.A	1B1_V2.4306.T.A	Newly Identified SNP
2F4R	CYP 1B1	4646	CYP1B1_60+1.4646.G.S	CYP1B1_60+1.4646.T.S	
2F4R	CYP 1B1	4668	1B1_4668.C.A	1B1_4668.G.A	Newly Identified SNP
2F4R	CYP 1B1	CNTRL	1B1.2F4R_A.X.S		Independent Amplicon Controls
2F4R	CYP 1B1	CNTRL	1B1.2F4R_B.X.S		Independent Amplicon Controls

SNP_ID	PROBE_ID
2E1_1772	CYP2E1_60.1772.C.A
2E1_1772	CYP2E1_60.1772.T.A
2E1_2019	CYP2E1_60.2019.C.S
2E1_2019	CYP2E1_60.2019.T.S
2E1_2754	CYP2E1_60.2754.G.S
2E1_2754	CYP2E1_60.2754.T.S
2E1_3085	CYP2E1_60.3085.A.A
2E1_3085	CYP2E1_60.3085.T.A
2E1_3104	CYP2E1_60.3104.A.A
2E1_3104	CYP2E1_60.3104.G.A
2E1_7592	CYP2E1_60.7592.A.S
2E1_7592	CYP2E1_60.7592.G.S
2E1_10456	CYP2E1_60.10456.A.S
2E1_10456	CYP2E1_60.10456.T.S
2E1_12720	CYP2E1_60.12720.C.S
2E1_12720	CYP2E1_60.12720.G.S
2E1_12847	CYP2E1_60.12847.A.S
2E1_12847	CYP2E1_60.12847.G.S
2E1_12945	CYP2E1_60.12945.C.A
2E1_12945	CYP2E1_60.12945.T.A
2D6_4802	CYP2D6_70.4802.A.S
2D6_4802	CYP2D6_70.4802.G.S
2D6_4896	CYP2D6_70.4896.C.S
2D6_4896	CYP2D6_70.4896.T.S
2D6_4907	CYP2D6_60.4907.A.S
2D6_4907	CYP2D6_60.4907.G.S
2D6_4907	CYP2D6_70.4907.A.S
2D6_4907	CYP2D6_70.4907.G.S
2D6_5447	CYP2D6_70.5447.A.A
2D6_5447	CYP2D6_70.5447.G.A
2D6_5472	CYP2D6_70.5472.A.S
2D6_5472	CYP2D6_70.5472.G.S
2D6_3595	CYP2D6_60.3595.A.A
2D6_3595	CYP2D6_60.3595.G.A
2D6_3595	CYP2D6_60.3595.A.S
2D6_3595	CYP2D6_60.3595.G.S
2D6_3597	CYP2D6_70.3597.C.S
2D6_3597	CYP2D6_70.3597.T.S
2D6_3598	CYP2D6_60.3598.C.A
2D6_3598	CYP2D6_60.3598.T.A
2D6_4089	CYP2D6_70.4089.C.S
2D6_4089	CYP2D6_70.4089.T.S
2D6_4099	CYP2D6_70.4099.C.S
2D6_4099	CYP2D6_70.4099.T.S
2D6_4102	CYP2D6_70.4102.G.A
2D6_4102	CYP2D6_70.4102.T.A
2D6_2642	CYP2D6_60.2642.C.S
2D6_2642	CYP2D6_60.2642.T.S
2D6_2642	CYP2D6_70.2642.C.S
2D6_2642	CYP2D6_70.2642.T.S
2D6_2658	CYP2D6_70.2658.C.A

Fig 8A

2D6_2658	CYP2D6_70.2658.T.A
2D6_3278	CYP2D6_60.3278.A.S
2D6_3278	CYP2D6_60.3278.G.S
2D6_3280	CYP2D6_60.3280.C.S
2D6_3280	CYP2D6_60.3280.G.S
2D6_3343	CYP2D6_70.3343.C.A
2D6_3343	CYP2D6_70.3343.T.A
2D6_1618	CYP2D6_70.1618.A.S
2D6_1618	CYP2D6_70.1618.G.S
2D6_1638	CYP2D6_70.1638.A.S
2D6_1638	CYP2D6_70.1638.G.S
2D6_1650	CYP2D6_70.1650.A.A
2D6_1650	CYP2D6_70.1650.G.A
2D6_1696	CYP2D6_70.1696.A.S
2D6_1696	CYP2D6_70.1696.G.S
2D6_1701	CYP2D6_70.1701.T.A
2D6_1701	CYP2D6_70.1701.C.A
2D6_1719	CYP2D6_60.1719.C.A
2D6_1719	CYP2D6_60.1719.T.A
2D6_1743	CYP2D6_70.1743.A.S
2D6_1743	CYP2D6_70.1743.G.S
2D6_2502	CYP2D6_60.2502.C.A
2D6_2502	CYP2D6_60.2502.G.A
2D6_2576	CYP2D6_60.2576.T.S
2D6_2576	CYP2D6_60.2576.C.S
2D6_2593	CYP2D6_60.2593.A.A
2D6_2593	CYP2D6_60.2593.C.A
2D6_2603	CYP2D6_70.2603.A.S
2D6_2603	CYP2D6_70.2603.G.S
2D6_2616	CYP2D6_60.2616.C.A
2D6_2616	CYP2D6_60.2616.G.A
2D6_3368	CYP2D6_70.3368.A.S
2D6_3368	CYP2D6_70.3368.G.S
2D6_3377	CYP2D6_70.3377.G.S
2D6_3377	CYP2D6_70.3377.T.S
2D6_3465	CYP2D6_60.3465.A.A
2D6_3465	CYP2D6_60.3465.G.A
2D6_3465	CYP2D6_60.3465.A.S
2D6_3465	CYP2D6_60.3465.G.S
2D6_3465	CYP2D6_70.3465.A.A
2D6_3465	CYP2D6_70.3465.G.A
2D6_3465	CYP2D6_70.3465.A.S
2D6_3465	CYP2D6_70.3465.G.S
2D6_3477	CYP2D6_60.3477.C.A
2D6_3477	CYP2D6_60.3477.T.A
2D6_3488	CYP2D6_60.3488.C.A
2D6_3488	CYP2D6_60.3488.T.A
2D6_3562	CYP2D6_60.3562.A.A
2D6_3562	CYP2D6_60.3562.G.A
2D6_4194	CYP2D6_70.4194.A.S
2D6_4194	CYP2D6_70.4194.C.S
2D6_4469	CYP2D6_60.4469.C.S

Fig. 8B

2D6_4469	CYP2D6_60.4469.T.S
2D6_4472	CYP2D6_70.4472.A.A
2D6_4472	CYP2D6_70.4472.C.A
2D6_4472	CYP2D6_70.4472.A.S
2D6_4472	CYP2D6_70.4472.C.S
2D6_4554	CYP2D6_70.4554.A.A
2D6_4554	CYP2D6_70.4554.C.A
2D6_4557	CYP2D6_70.4557.C.S
2D6_4557	CYP2D6_70.4557.T.S
2D6_4558	CYP2D6_70.4558.A.A
2D6_4558	CYP2D6_70.4558.G.A
2D6_5496	CYP2D6_70.5496.C.S
2D6_5496	CYP2D6_70.5496.G.S
2D6_5506	CYP2D6_60.5506.C.A
2D6_5506	CYP2D6_60.5506.T.A
2D6_5661	CYP2D6_70.5661.A.S
2D6_5661	CYP2D6_70.5661.G.S
2D6_5734	CYP2D6_70.5734.C.A
2D6_5734	CYP2D6_70.5734.T.A
2D6_5799	CYP2D6_60.5799.C.S
2D6_5799	CYP2D6_60.5799.G.S
2E1_1627	CYP2E1_60.1627.C.A
2E1_1627	CYP2E1_60.1627.G.A
3A4_816	CYP3A4_60.816.G.S
3A4_816	CYP3A4_60.816.A.S
3A4_918	CYP3A4_60.918.A.S
3A4_918	CYP3A4_60.918.G.S
2C19_430	CYP2C19EXONS_70.430.C.A
2C19_430	CYP2C19EXONS_70.430.T.A
2C19_636	CYP2C19EXONS_60.636.A.S
2C19_636	CYP2C19EXONS_60.636.G.S
2C19_681	CYP2C19EXONS_60.681.A.S
2C19_681	CYP2C19EXONS_60.681.G.S
1B1_4160	CYP1B1_60.4160.G.A
1B1_4160	CYP1B1_60.4160.T.A
1B1_7973	CYP1B1_60.7973.C.A
1B1_7973	CYP1B1_60.7973.T.A
1B1_7996	CYP1B1_60.7996.A.S
1B1_7996	CYP1B1_60.7996.G.S
1B1_8006	CYP1B1_60.8006.A.S
1B1_8006	CYP1B1_60.8006.G.S
1B1_8195	CYP1B1_60.8195.A.A
1B1_8195	CYP1B1_60.8195.G.A
1B1_8242	CYP1B1_60.8242.C.S
1B1_8242	CYP1B1_60.8242.T.S
1B1_8587	CYP1B1_60.8587.C.S
1B1_8587	CYP1B1_60.8587.G.S
1A1_1223	CYP1A1_60.1223.C.A
1A1_1223	CYP1A1_60.1223.T.A
2D6_3326	2D6_66.3326.G.A
2D6_3326	2D6_66.3326.T.A
2D6_3326	2D6_66.3326.G.S

Fig 8C

2D6_3326	2D6_66.3326.T.S
2D6_4168	2D6_66.4168.A.A
2D6_4168	2D6_66.4168.C.A
2D6_4168	2D6_66.4168.A.S
2D6_4168	2D6_66.4168.C.S
1A1_6568	CYP1A1_60.6568.A.A
1A1_6568	CYP1A1_60.6568.C.A
1A1_6568	CYP1A1_60.6568.A.S
1A1_6568	CYP1A1_60.6568.C.S
1A1_6570	CYP1A1_60.6570.A.A
1A1_6570	CYP1A1_60.6570.G.A
1A2_2640	CYP1A2_60.2640.A.A
1A2_2640	CYP1A2_60.2640.C.A
1A2_2866	CYP1A2_60.2866.C.S
1A2_2866	CYP1A2_60.2866.G.S
1B1_3793	CYP1B1_60.3793.C.A
1B1_3793	CYP1B1_60.3793.T.A
1B1_3793	CYP1B1_60.3793.C.S
1B1_3793	CYP1B1_60.3793.T.S
1B1_3947	CYP1B1_60.3947.C.S
1B1_3947	CYP1B1_60.3947.G.S
1B1_3976	CYP1B1_60.3976.C.S
1B1_3976	CYP1B1_60.3976.G.S
1B1_3987	CYP1B1_60.3987.A.A
1B1_3987	CYP1B1_60.3987.G.A
1B1_8807	CYP1B1_60.8807.A.S
1B1_8807	CYP1B1_60.8807.T.S
2C19_276	CYP2C19EXONS_70.276.C.A
2C19_276	CYP2C19EXONS_70.276.G.A
2C19_395	CYP2C19EXONS_70.395.A.A
2C19_395	CYP2C19EXONS_70.395.G.A
	CONTROL PROBES
	PBR322WSNPS,4056.C.S
	PBR322WSNPS,4056.T.S
	WIAF-1648.107.A.A
	WIAF-1648.107.G.A
	WIAF-198.38.C.A
	WIAF-198.38.T.A
	2D7PSEUDOGENECONTROL_60.111.C.A
	2D7PSEUDOGENECONTROL_60.111.G.A
	2D7PSEUDOGENECONTROL_60.111.C.S
	2D7PSEUDOGENECONTROL_60.111.G.S
	2D7APSEUDOGENECONTROL_60.23.A.A
	2D7APSEUDOGENECONTROL_60.23.G.A
	2D7APSEUDOGENECONTROL_60.2370.A.S
	2D7APSEUDOGENECONTROL_60.2370.G.S
	2D7APSEUDOGENECONTROL_60.2592.C.S
	2D7APSEUDOGENECONTROL_60.2592.T.S
	2D7APSEUDOGENECONTROL_60.3471.C.A
	2D7APSEUDOGENECONTROL_60.3471.T.A
	2D7PSEUDOGENECONTROL_60.600.G.S

Fig 8D

	2D7PSEUDOGENECONTROL_60.600.T.S
	2D7PSEUDOGENECONTROL_60.1760.C.S
	2D7PSEUDOGENECONTROL_60.1760.T.S
	2D7PSEUDOGENECONTROL_60.2108.A.S
	2D7PSEUDOGENECONTROL_60.2108.G.S
	2D7B_60.3539.G.S
	2D7B_60.3539.T.S
	2D7B_60.3647.A.A
	2D7B_60.3647.G.A
	2D7B_60.3768.A.S
	2D7B_60.3766.C.S
	2D7B_60.4506.C.S
	2D7B_60.4506.G.S
	2D8_60.105.A.A
	2D8_60.105.G.A
	2D8_60.3080.A.S
	2D8_60.3080.G.S
	2D7PSEUDOGENECONTROL_60.1360.C.S
	2D7PSEUDOGENECONTROL_60.1360.T.S
	2D7PSEUDOGENECONTROL_60.3030.A.S
	2D7PSEUDOGENECONTROL_60.3030.G.S
	2D7PSEUDOGENECONTROL_60.3148.A.S
	2D7PSEUDOGENECONTROL_60.3148.G.S
	2D7B_60.442.C.A
	2D7B_60.442.T.A
	2D7B_60.652.G.S
	2D7B_60.652.T.S
	2D7B_60.1185.G.S
	2D7B_60.1185.T.S
	2D7B_60.1316.A.A
	2D7B_60.1316.C.A
	2D7B_60.1671.A.A
	2D7B_60.1671.T.A
	2D7B_60.3172.C.S
	2D7B_60.3172.G.S
	2D8_60.3181.A.A
	2D8_60.3181.G.A
	2D8_60.4120.A.A
	2D8_60.4120.G.A
	2D8_60.4199.C.A
	2D8_60.4199.T.A
	2D8_60.4223.C.S
	2D8_60.4223.T.S
	2D8_60.4750.C.A
	2D8_60.4750.G.A

Fig 8E

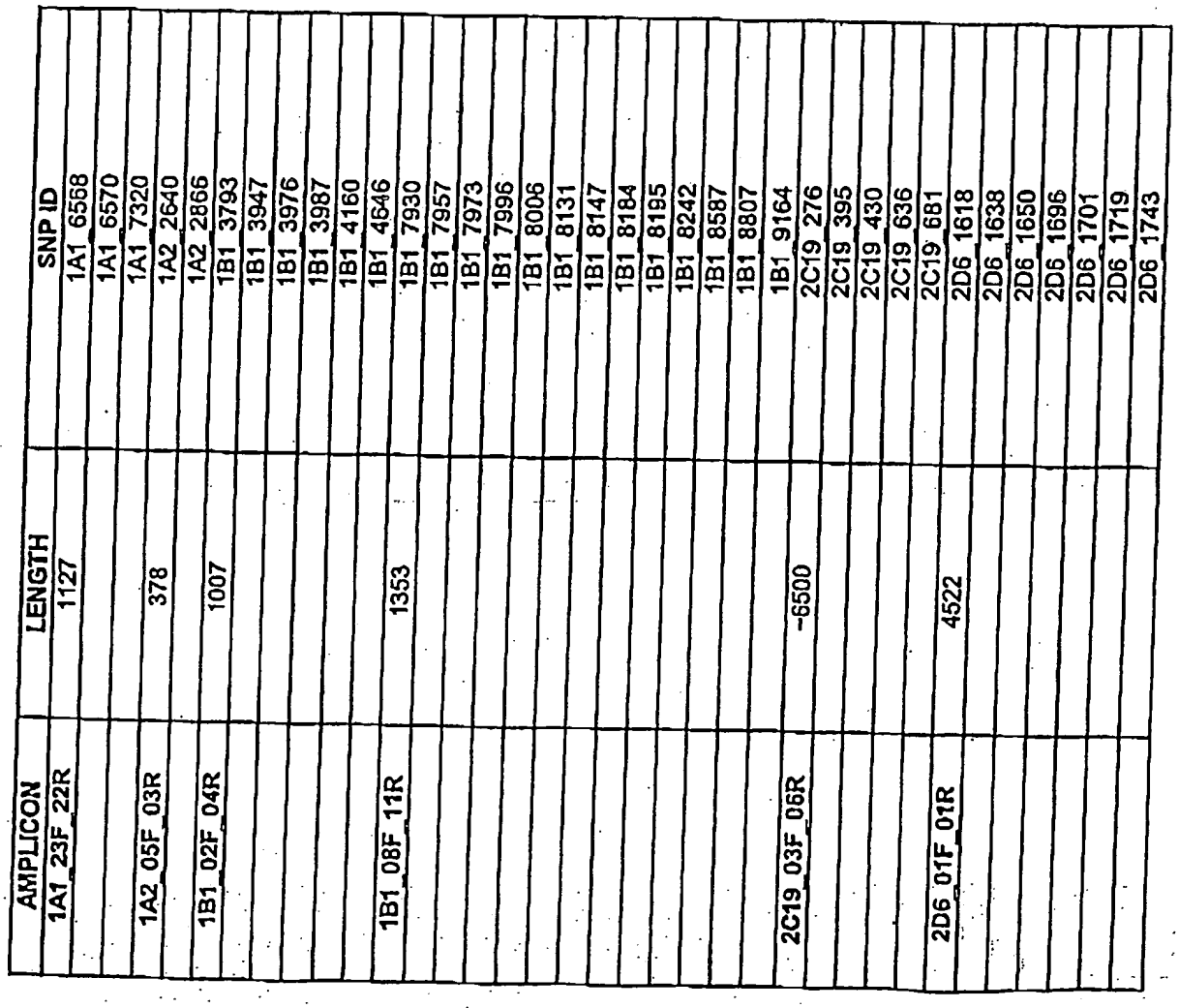
GENE	RELATED/ MAPPED TOGETHER	DNA/mRNA/Partials	ACCESSION #
2D6	2D6	gDNA	M33388
	2D7	gDNA	M33387
	2D7A	gDNA	X58467
	2D7B	gDNA	X58468
	2D8	gDNA	M33387
2E1	2E1	gDNA	J02843
3A4	3A4	Partial	D11131
		gDNA	AF209389
3A5	3A5	gDNA	AC005020
		mRNA	NM_000777
	3A5P	Splice Variant (mRNA)	L26985
1A1	1A1	gDNA	X04300
		gDNA	X02612
		Partial	D12525
1A2	1A2	Partial gDNA	M31664
		Partial gDNA	M31665
		Partial gDNA	M31666
		Partial gDNA	M31667
1B1	1B1	gDNA	U56438
2C9	2C9	mRNA	M61855
	2C9	Partial gDNA	L16877
	2C9	Partial gDNA	L16878
	2C9	Partial gDNA	L16879
	2C9	Partial gDNA	L16880
	2C9	Partial gDNA	L16881
	2C9	Partial gDNA	L16882
	2C9	Partial gDNA	L16883

Fig 9A

Fig 9B

GENE	RELATED/ MAPPED TOGETHER	DNA/mRNA/Partials	ACCESSION #
	2C19	mRNA	NM_000769
	2C19	Draft gDNA (Exons 8-9)	AL133513
	2C18	mRNA	M61856
	2C8	mRNA	NM_000770
2C19	2C19	mRNA	NM_000769
	2C19	Partial gDNA (Exons 8-9)	AL133513
	2C9	mRNA	M61855
	2C9	Partial gDNA	L16877
	2C9	Partial gDNA	L16878
	2C9	Partial gDNA	L16879
	2C9	Partial gDNA	L16880
	2C9	Partial gDNA	L16881
	2C9	Partial gDNA	L16882
	2C9	Partial gDNA	L16883
	2C18	mRNA	M61856
	2C8	mRNA	NM_000770

Fig 10A



AMPLICON	LENGTH	SNP ID
1A1_23F_22R	1127	1A1_6568
		1A1_6570
1A2_05F_03R	378	1A1_7320
		1A2_2640
1B1_02F_04R	1007	1A2_2866
		1B1_3793
		1B1_3947
		1B1_3976
		1B1_3987
		1B1_4160
1B1_08F_11R	1353	1B1_4646
		1B1_7930
		1B1_7957
		1B1_7973
		1B1_7996
		1B1_8006
		1B1_8131
		1B1_8147
		1B1_8184
		1B1_8195
		1B1_8242
		1B1_8587
		1B1_8807
2C19_03F_06R	~6500	1B1_9164
		2C19_276
		2C19_395
		2C19_430
		2C19_636
		2C19_681
2D6_01F_01R	4522	2D6_1618
		2D6_1638
		2D6_1650
		2D6_1696
		2D6_1701
		2D6_1719
		2D6_1743

Fig 10B

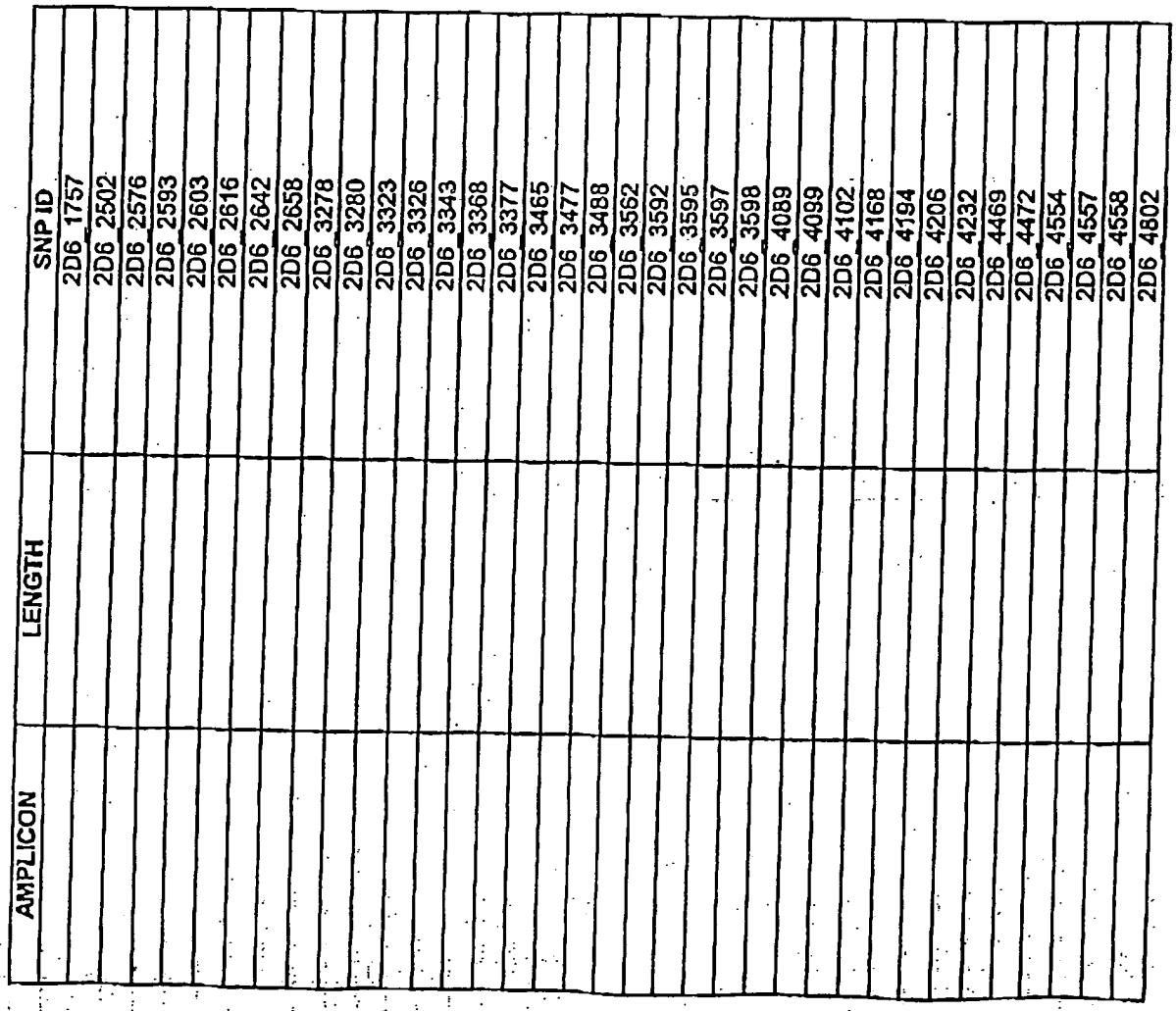

AMPLICON
LENGTH
SNP ID
2D6_1757
2D6_2502
2D6_2576
2D6_2593
2D6_2603
2D6_2616
2D6_2642
2D6_2658
2D6_3278
2D6_3280
2D6_3323
2D6_3326
2D6_3343
2D6_3368
2D6_3377
2D6_3465
2D6_3477
2D6_3488
2D6_3562
2D6_3592
2D6_3595
2D6_3597
2D6_3598
2D6_4089
2D6_4099
2D6_4102
2D6_4168
2D6_4194
2D6_4206
2D6_4232
2D6_4469
2D6_4472
2D6_4554
2D6_4557
2D6_4558
2D6_4802

Fig 10C

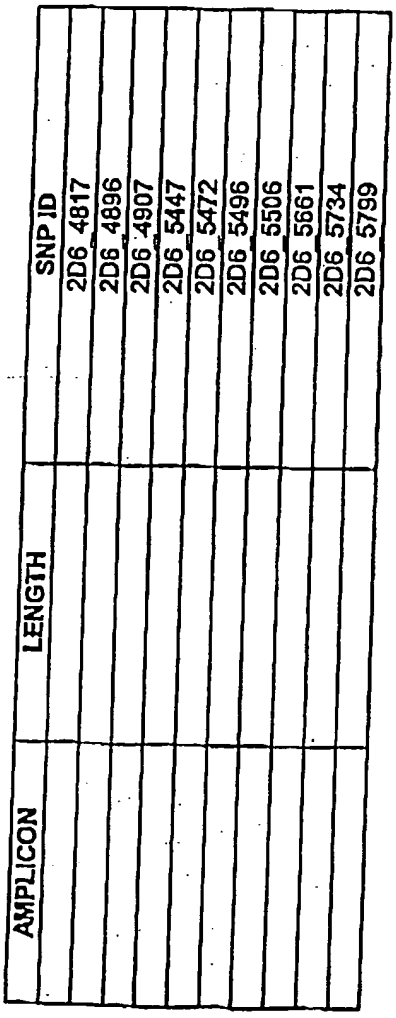

AMPLICON
LENGTH
SNP ID
2D6_4817
2D6_4896
2D6_4907
2D6_5447
2D6_5472
2D6_5496
2D6_5506
2D6_5661
2D6_5734
2D6_5799

Fig 11 The Codelink™ SNP Bioassay for human cytochrome P450 genes.

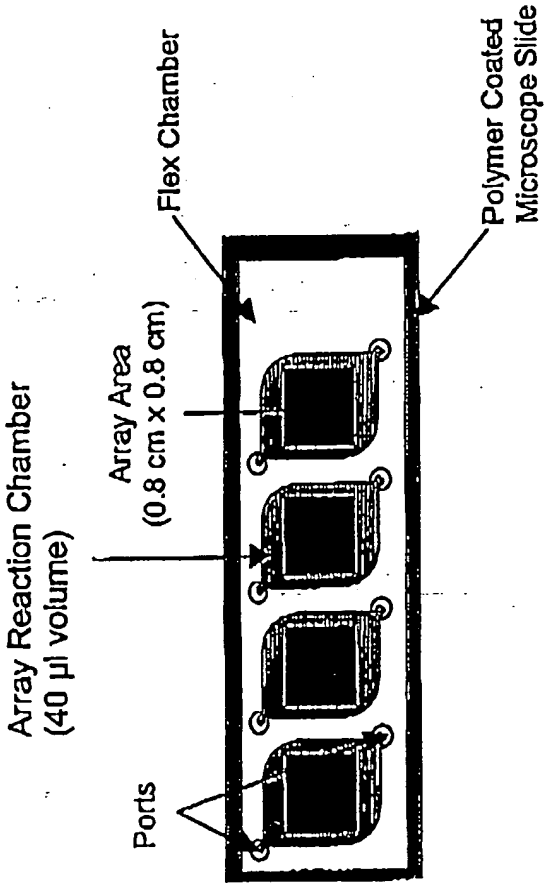
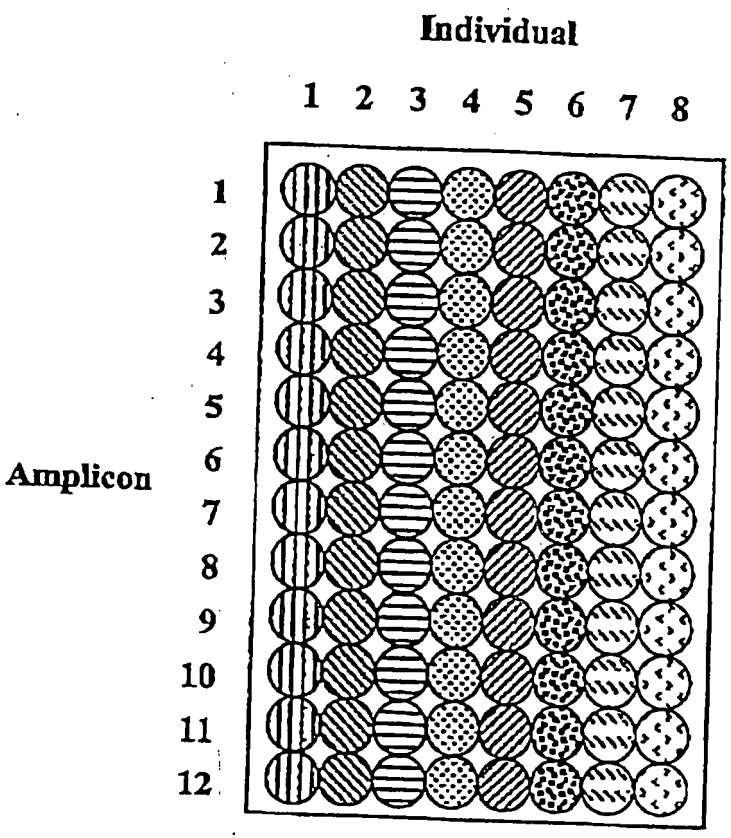


Fig 12 Layout of primer pairs in primer plates.



NOTE: Each sample individual will be aliquoted across 12 separate PCR reactions.

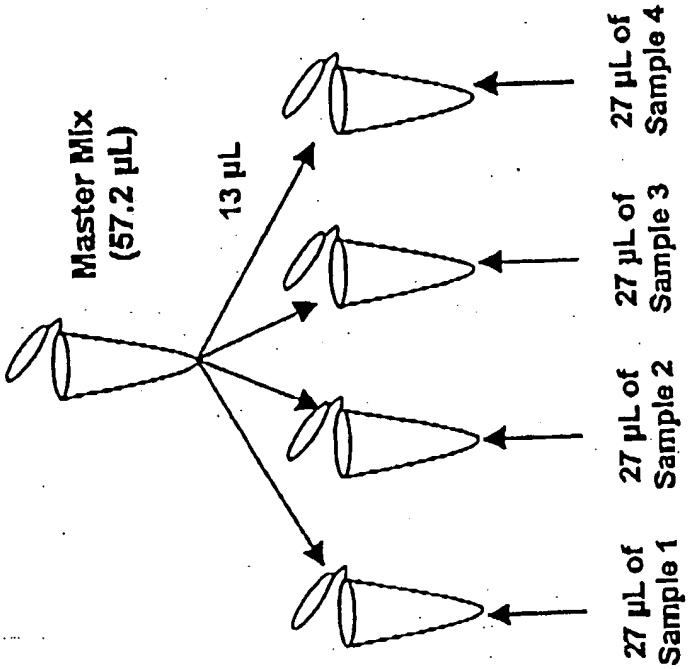


Fig 13. Addition of master mix and samples to microfuge tubes.

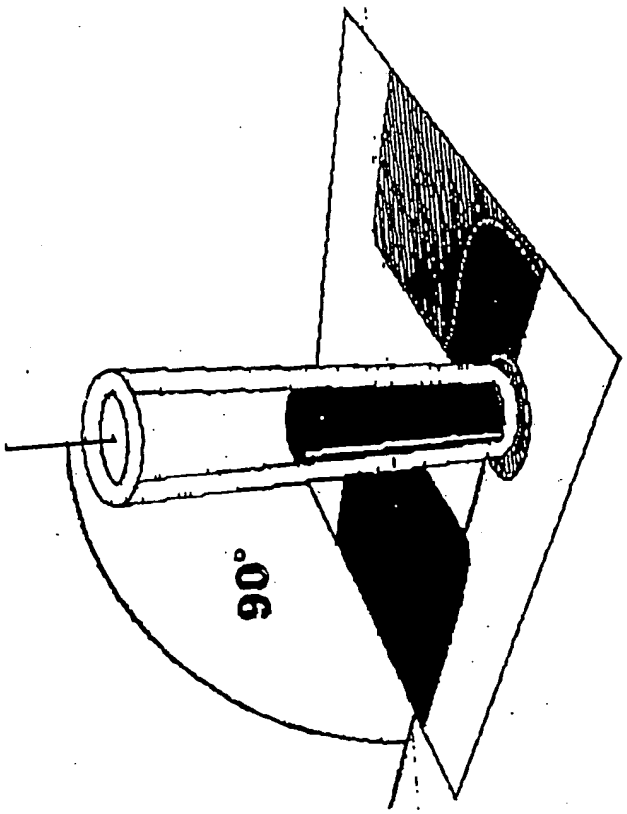


Fig 14 Tip orientation for loading reaction mixtures into chambers.

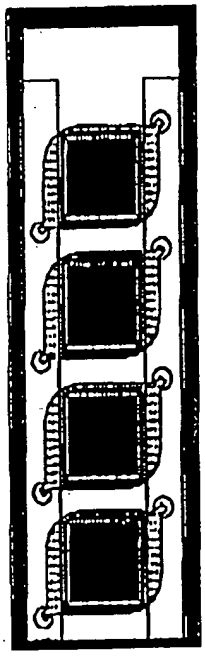


Fig 15 Orientation of sealing strips over chamber ports.

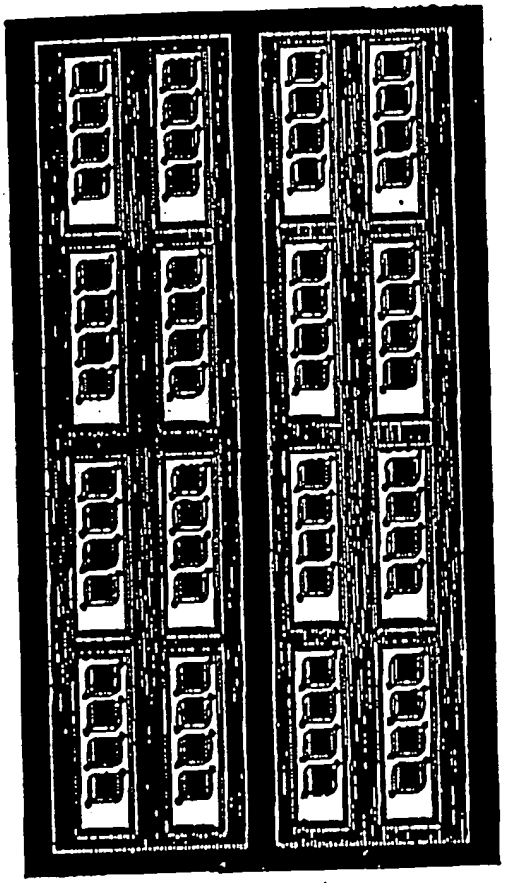


Fig 16. Slide placement on the Hybaid Omnislide heat blocks.

Fig 17

Fig 17 : Prevention of self-extension due to base additions.

Target-Independent signal strength	Probe	Probe Sequence (5' to 3')	Length/#GC	Predicted Stem-Loop	Predicted Base Extended	Observed Base Extended
Strong	50APOE321.T.A	TACACTGCCAGGCA	14/8	TGCCAGGCA	G	G
Strong	60MAP913.114.T.A	TCTCTGTCTGTCTCTTGCCA	20/10	TGTCTCTTGGCA	G	G
Strong	80POMCC7111G.111.C.A	AAGTGCTCCATGGAGTAGGAG	21/11	CTCC (8) GGAG	C	C
Strong	70POMCC7111G.111.C.S	CGCCAGGCCAAGCGC	15/12	GCG (8) CGC	G	G
Strong	70.LP.2.150.C.A	CCCAGAATGCTCACCAGCCTG	21/13	CAGCCTG	G	G
Strong	60.MAP286.173.C.S	CCCAGCCAATTTTATTTGC	19/8	GCAA (6) TTGC	C	C
Strong	APOE182.A.A	CAGCGCGCCGCT	12/10	GCGCG CGCGT	T	G>C

Table 4 Examples of probe sequences that show a strong target-independent signal in the SBE assay. The predicted stem-loop region is underlined.

Fig 18

Fig 19

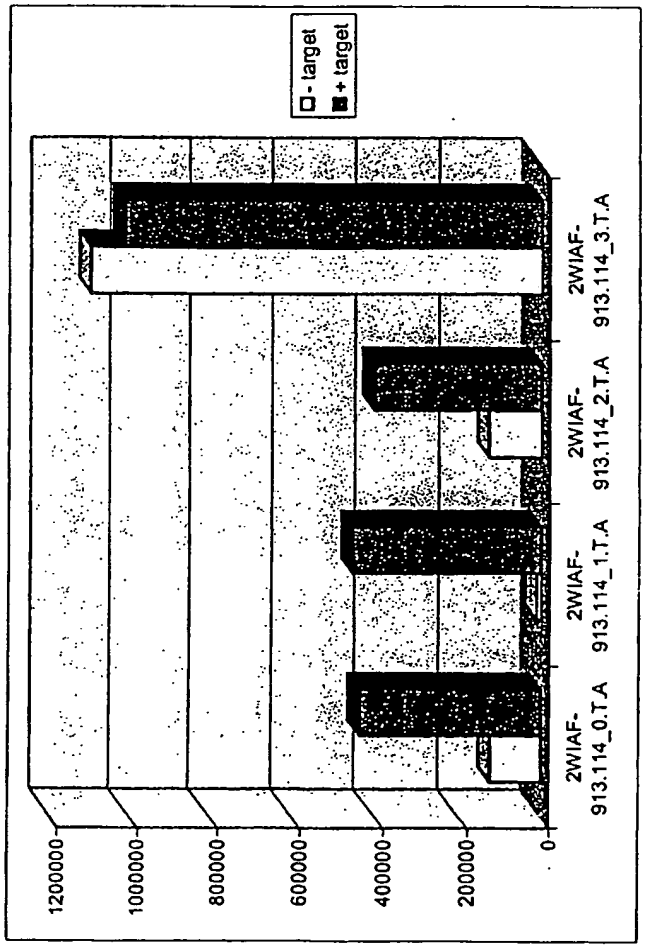
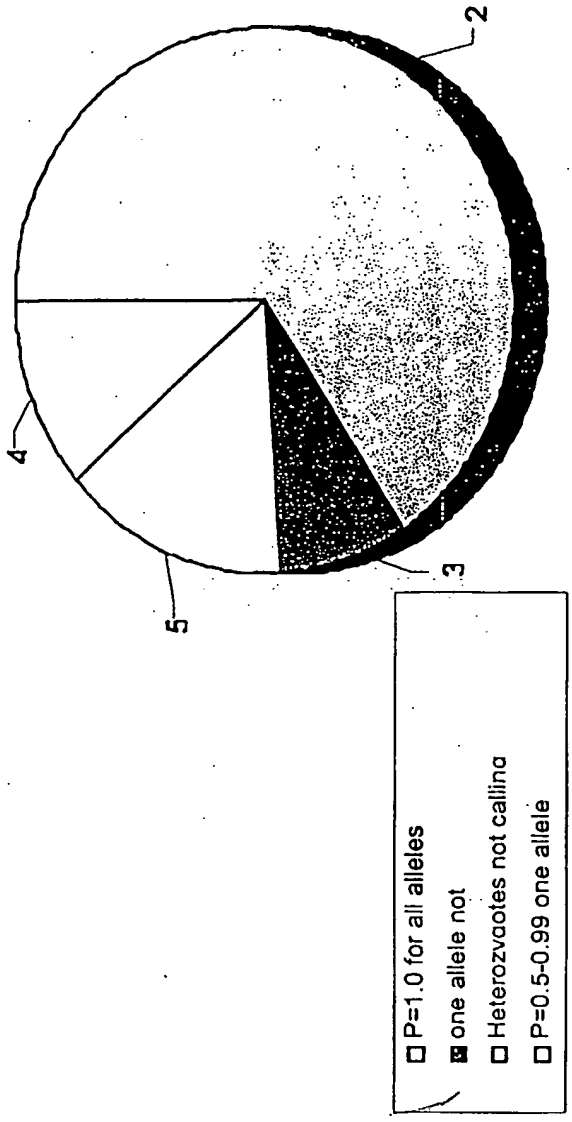

- target
+ target
1200000
1000000
800000
600000
400000
200000
0
2WIAF-913.114_0.T.A
2WIAF-913.114_1.T.A
2WIAF-913.114_2.T.A
2WIAF-913.114_3.T.A

Fig 20


2
3
4
5
P=1.0 for all alleles
one allele not
Heterozygotes not calling
P=0.5-0.99 one allele

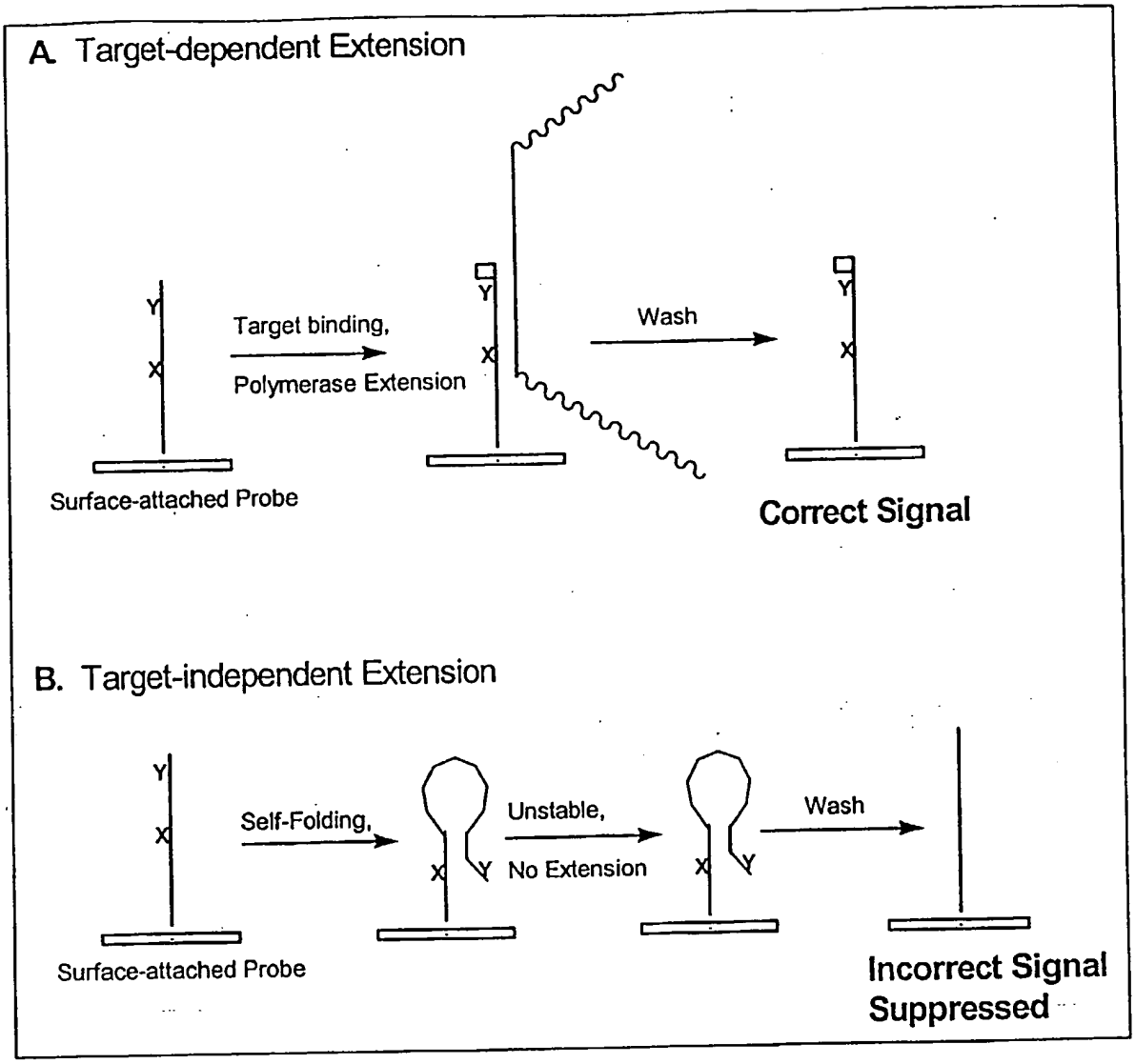
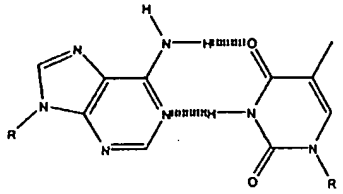

A. Target-dependent Extension
Y
X
Target binding,
Polymerase Extension
Y
X
Wash
Y
X
Surface-attached Probe
Correct Signal
B. Target-independent Extension
Y
X
Surface-attached Probe
Self-Folding,
X
Y
Unstable,
No Extension
X
Y
Wash
Incorrect Signal
Suppressed

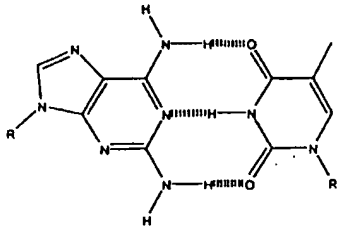
Fig 21

A. Natural A:T base-pair,
pairs equally well with target and itself



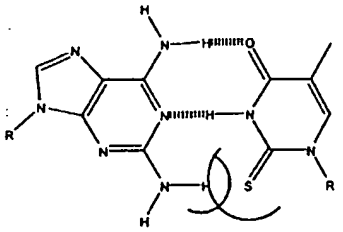
A T

C. 2-am-A:T base-pair, (target-probe pair)
forms a very stable base-pair



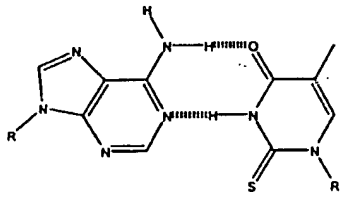
2-am-A T

B. Non-natural 2-am-A:2-thioT base-pair,
does not form a stable base-pair



2-am-A 2-thio-T

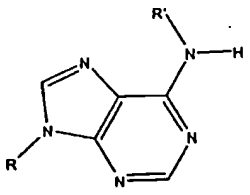
D. A:2-thio-T base-pair, (target-probe pair)
forms a stable base-pair



A 2-thio-T

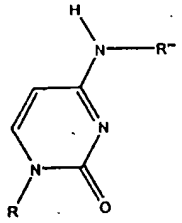
Fig 22

A. Exo-cyclic amine modified A



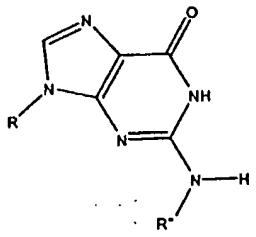
Modified A

A. Exo-cyclic amine modified C



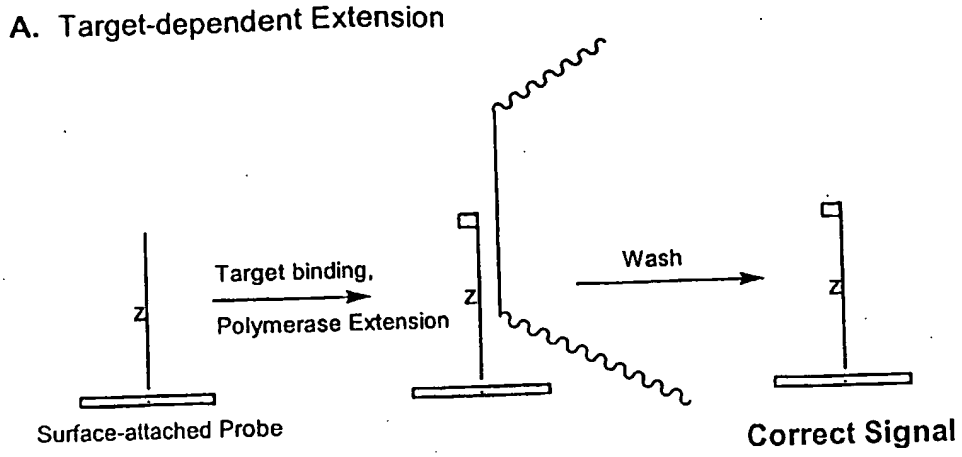
Modified C

B. Exo-cyclic amine modified G



Modified G

Fig 23


A. Target-dependent Extension
Z
Target binding,
Polymerase Extension
Z
Wash
Z
Surface-attached Probe
Correct Signal

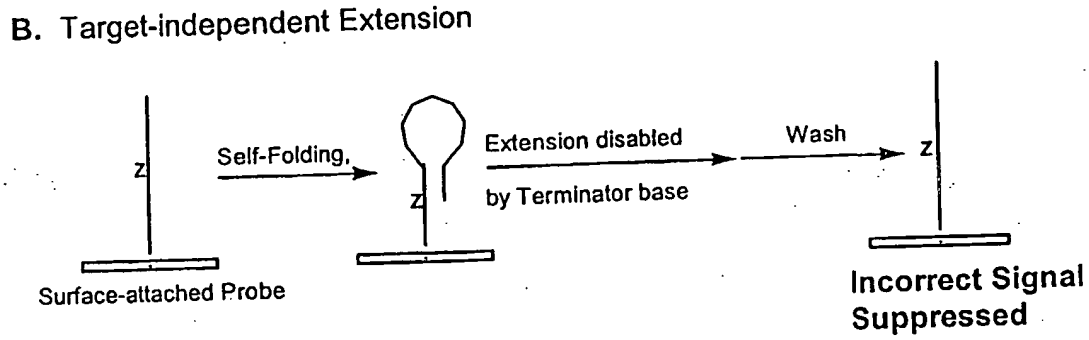
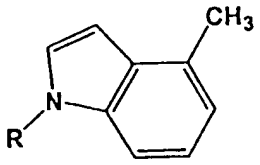

B. Target-independent Extension
Z
Self-Folding,
Z
Extension disabled
by Terminator base
Wash
Z
Surface-attached Probe
Incorrect Signal
Suppressed

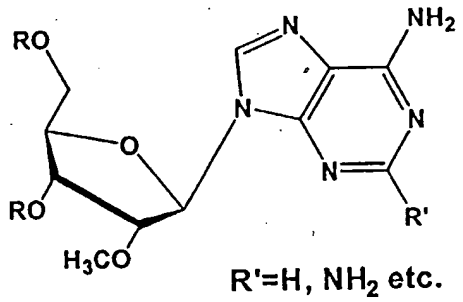
Fig 24

A. "Terminator" base



4-methyl-indole

B. "Terminator" nucleoside



2'-O-methyl-2-amino-A

Fig 25

Fig 26

Table 6 List of modified bases/nucleosides used.

Q = abasic nucleotide: no base-pairing ability, no stacking energy; placed immediately downstream of putative stem-loop; expect A to be incorporated when Q is in template (the "A rule").

I = 4-methylindole: A analog; placed immediately downstream of putative stem-loop; terminates DNA polymerase activity.

K = 5-nitroindole: universal base; placed immediately downstream of putative stem-loop; does not form base pairs but contributes stacking energy.

Z = 2-amino-A: placed within the stem of putative stem-loop; forms 3 hydrogen-bonds with T; no base pairing with 2-thio-dT.

X = 2-thio-dT: placed with stem of putative stem-loop; stable base pairs with A; no base pairing with 2-amino-A.

Fig 26

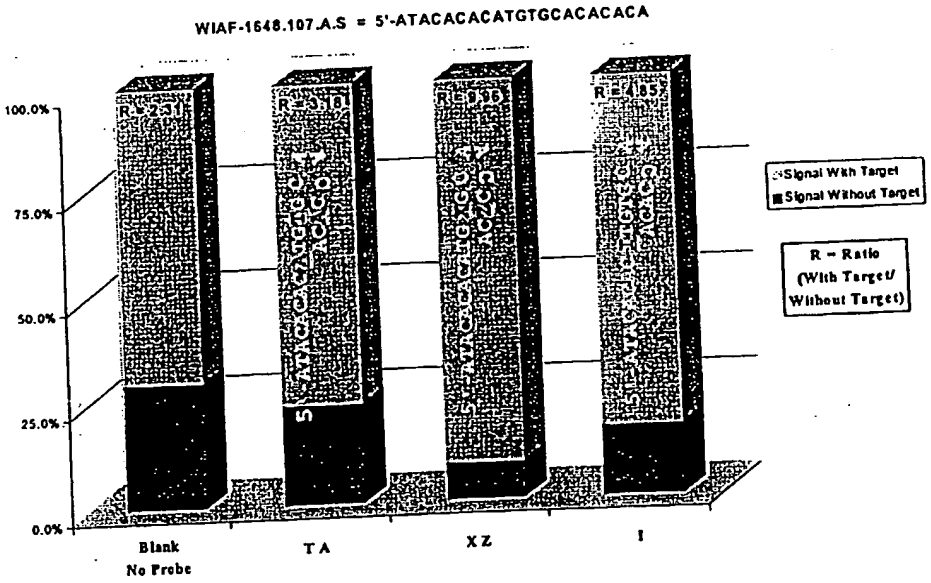

WIAF-1648.107.A.S = 5'-ATACACACATGTGCACACACA
100.0%
75.0%
50.0%
25.0%
0.0%
R = 2.51
R = 4.30
R = 0.16
R = 4.85
Signal With Target
Signal Without Target
R = Ratio (With Target/ Without Target)
Blank No Probe
T A
X Z
I

Fig 27

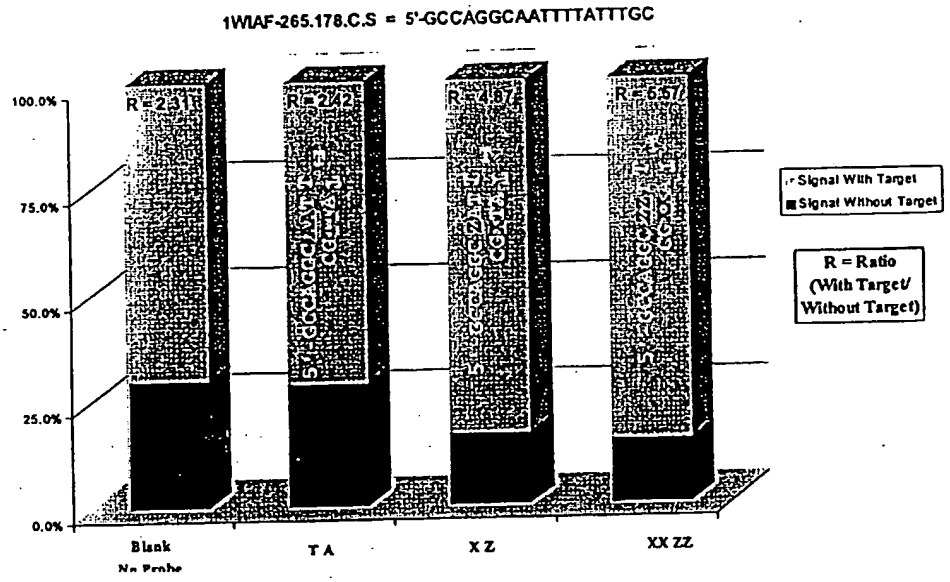

1WIAF-265.178.C.S = 5'-GCCAGGCAATTTTATTTGC
100.0%
75.0%
50.0%
25.0%
0.0%
R = 2.31
R = 2.42
R = 4.97
R = 6.57
Signal With Target
Signal Without Target
R = Ratio (With Target/ Without Target)
Blank
No Probe
T A
X Z
XX ZZ

Fig 28

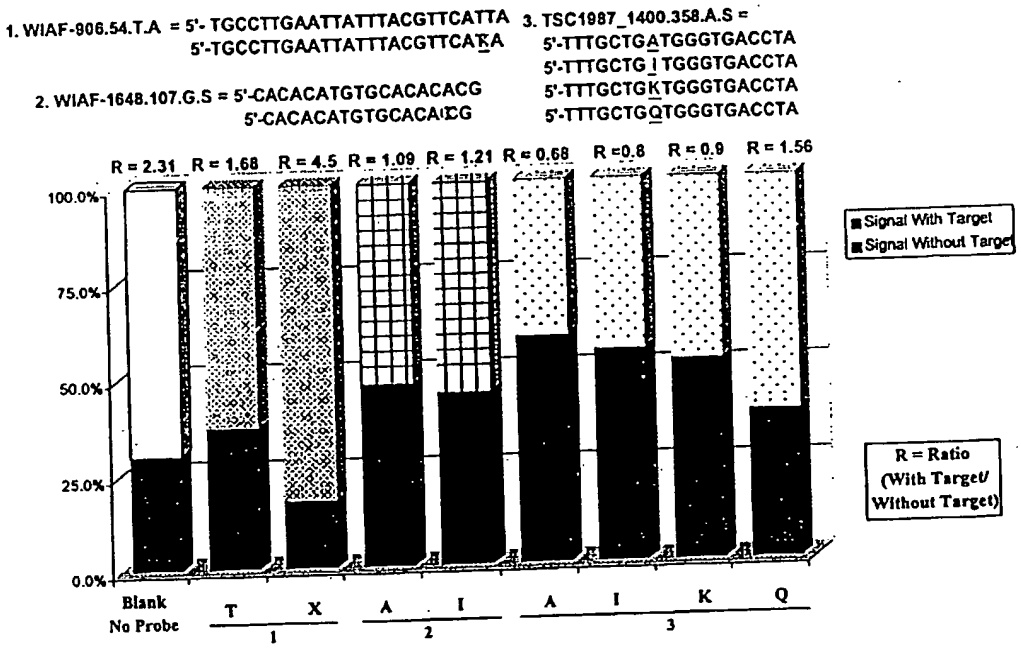

1. WIAF-806.54.T.A = 5'- TGCCTTGAATTATTTACGTTCATTA
5'-TGCCTTGAATTATTTACGTTCAXA
2. WIAF-1648.107.G.S = 5'-CACACATGTGCACACACG
5'-CACACATGTGCACAIΣG
3. TSC1987_1400.358.A.S =
5'-TTTGCTGATGGGTGACCTA
5'-TTTGCTG I TGGGTGACCTA
5'-TTTGCTGKTGGGTGACCTA
5'-TTTGCTGQTGGGTGACCTA
R = 2.31 R = 1.68 R = 4.5 R = 1.09 R = 1.21 R = 0.68 R =0.8 R = 0.9 R = 1.56
100.0%
75.0%
50.0%
25.0%
0.0%
Signal With Target
Signal Without Target
R = Ratio (With Target/ Without Target)
Blank No Probe
T X A I A I K Q
1 2 3

Fig 29

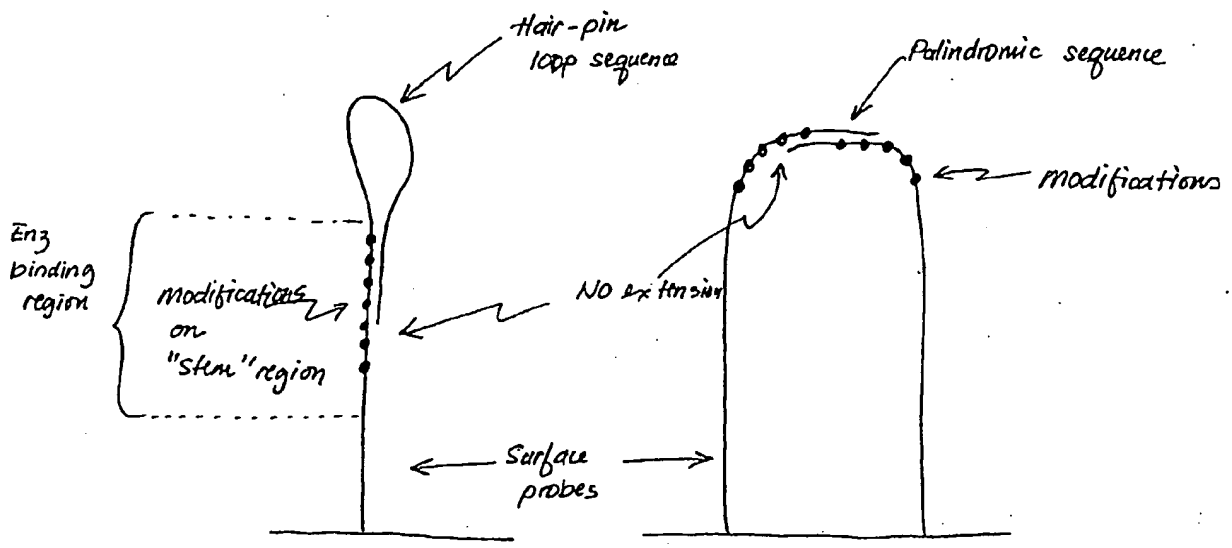
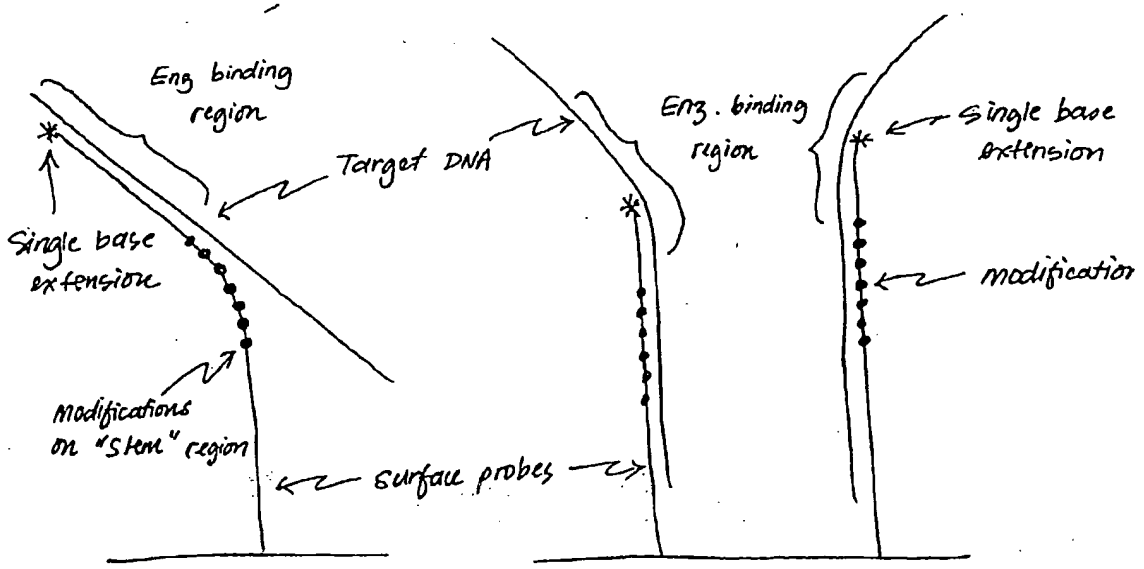


Fig 30

Self-extension inhibited due to modifications on bases in the "stem" region that prevent extension enzyme from binding.

Fig 31



Extension due to probe – target hybridization is not inhibited.

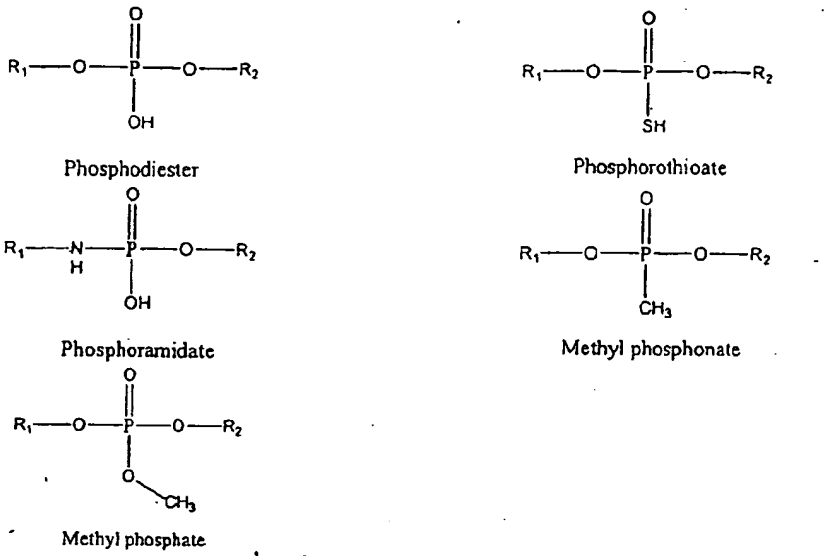


Fig 32A modified nucleotide bases reduces the binding affinity of the SBE enzyme or extension enzyme

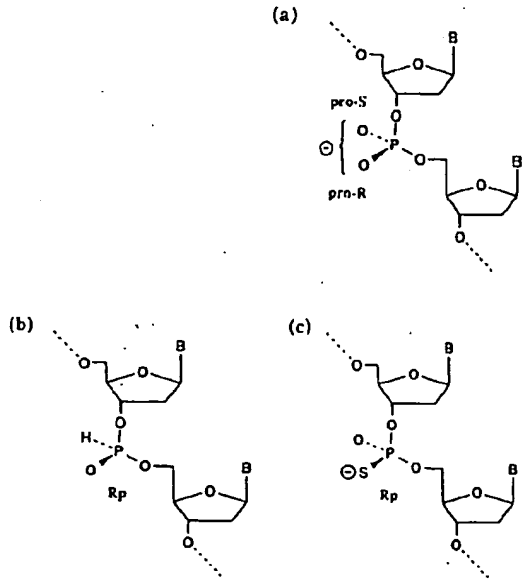


Fig 32B : Chiral phosphodiester analogues.

Fig 33

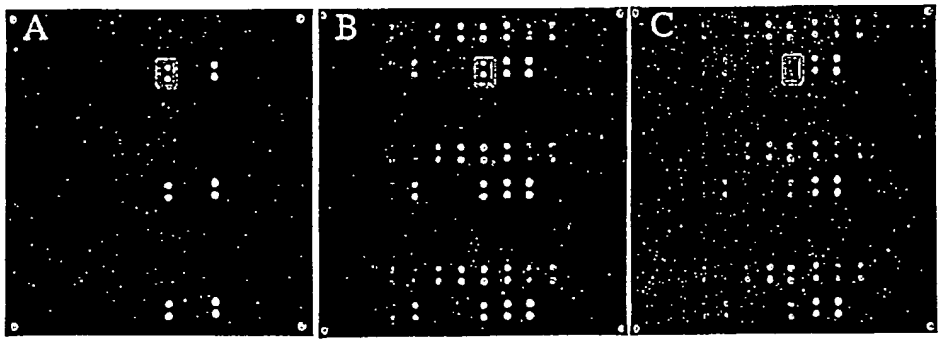


Fig 33 Results from an experiment using oligonucleotide inhibitors to prevent self extension probes in the SBE assay.

Method for uniplexed target prep for SNP genotyping and primer extension without self-extension

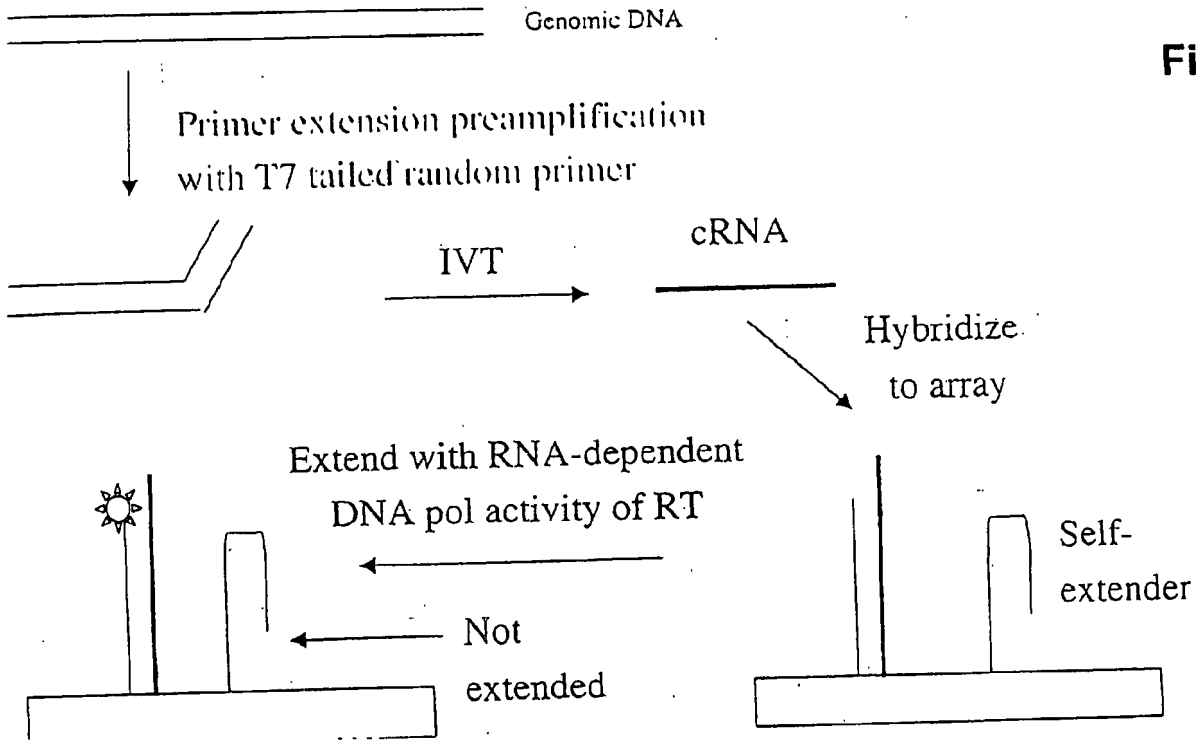


Fig 34

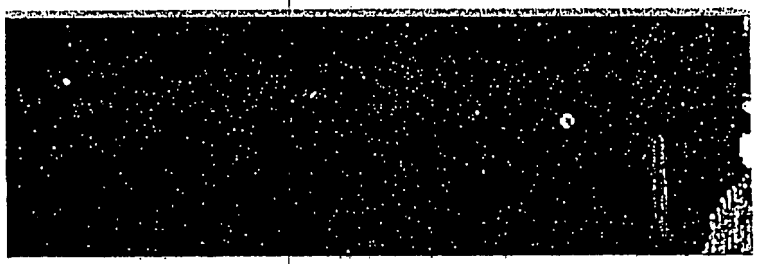
Fig 35

Controls

Enzyme

rTth, Modified Reverse transcriptase

Non-extender **Self-extender**

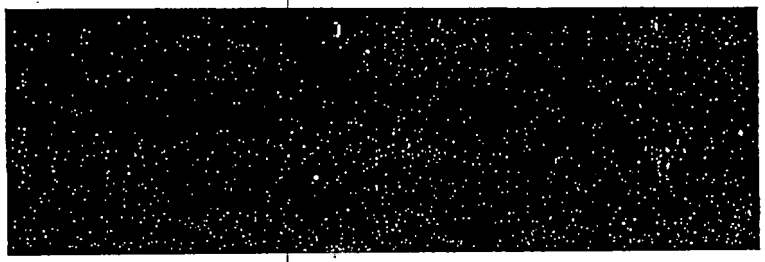


- cRNA + cRNA

RESULTS

The self-extender shows signal only in presence of cRNA

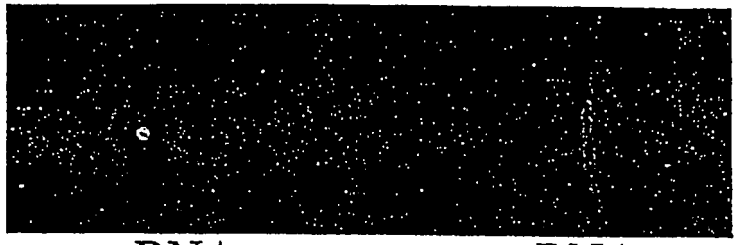
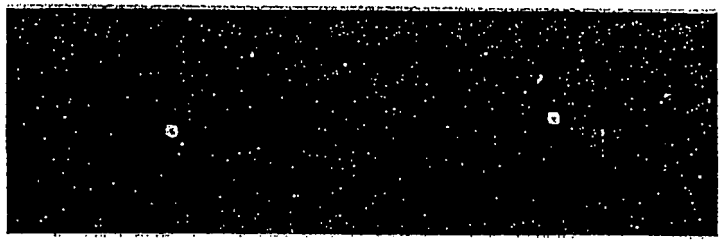
Bacterial probe **Bacterial probe**



- cRNA + cRNA

The signal is human specifi since bacterial probes do not show signal with the human cRNA

Fig 36

Enzyme	Non-extender / Self-extender	RESULTS
Modified Reverse Transcriptase Enzyme (rTth)	 + cRNA - cRNA	Modified Enzyme Eliminates Self-extension
Regular Reverse Transcriptase (Superscript II)	 + cRNA - cRNA	Self-extension Seen with Regular Enzyme

Reaction of Amino Oligonucleotides on the SurModics Surface

(an example of acyl substitution reaction on the polymer backbone)

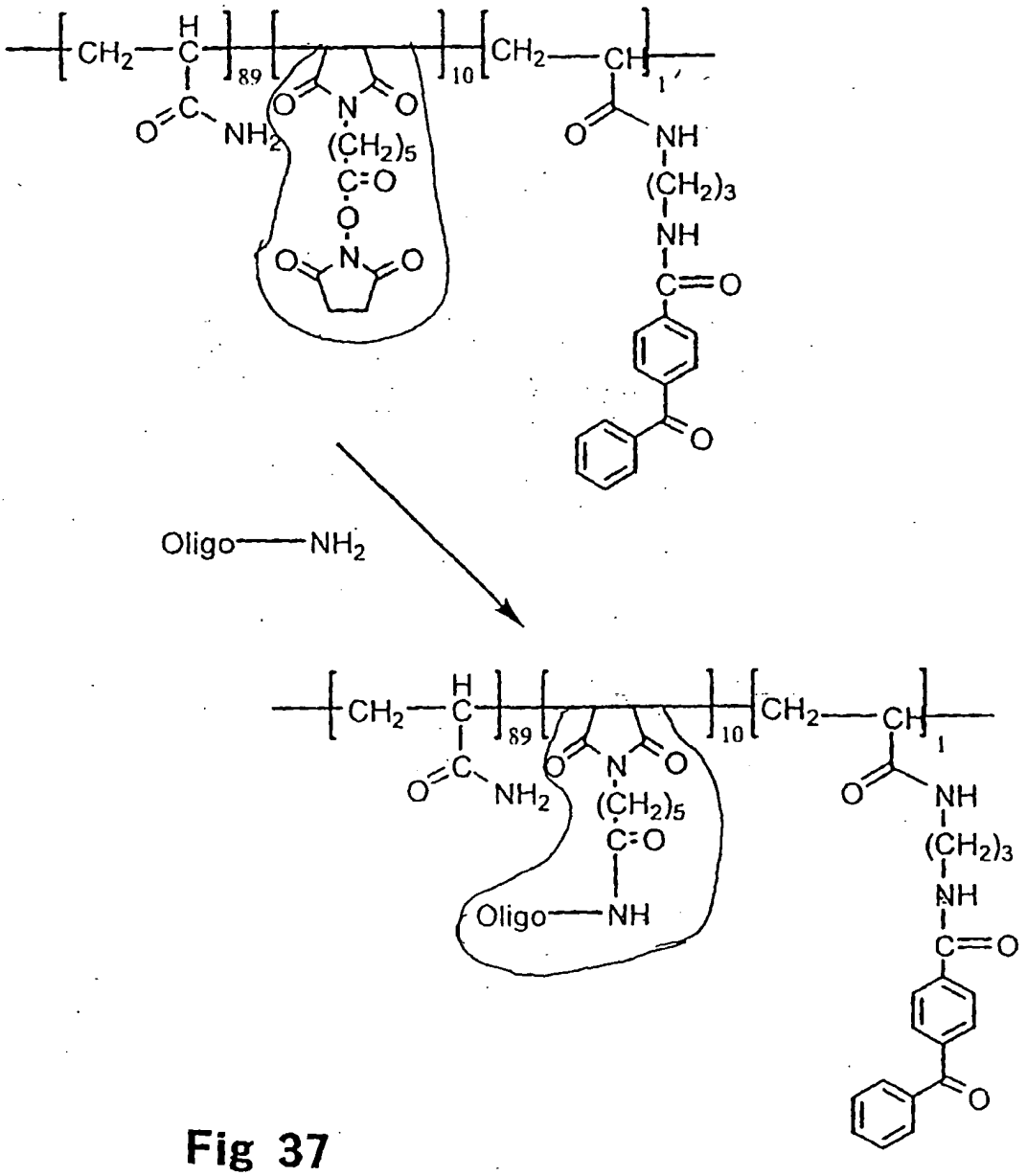
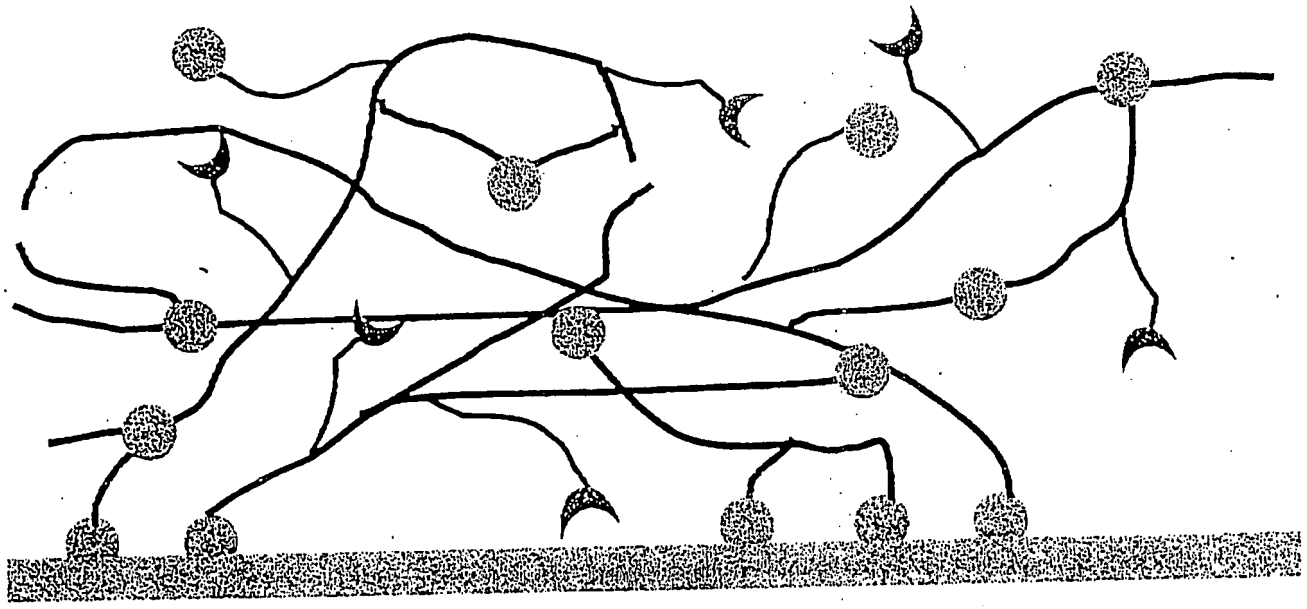


Fig 37

Possible Structure of a SurModics Gel Matrix



Polyacrylamide
80~ 90 %

Photocrosslinker
1 ~ 2 %

Oligo attachment
function group
~ 10 %

Fig 38

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